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Gupta, Anish Thursday, March 14, 2002 10:34 AM STIC-Biotech/ChemLib

Search Request:

Serial Number 09/544,665 Art Unit: 1653

Please search Seq. ID 1-5.

thank you anish gupta

Date: 3-15-02 Location: 9A13 (mailbox in 9B01)

Point of Contact: Mona Smith Technical Information Specialist CM1 6A01 Tel: 308-3279

Point of Contact: Mona Smith Technical Information Specialist CM1 6A01 Tel: 308-3278

Searcher: M. Smith
Phone:
Location:
Date Picked Up: 3/15/02
Date Completed: 3109602
Searcher Prep/Review: _/5
Clerical:
Online time: /5

TYPE OF SEARCH:
NA Sequences:
AA Sequences: 5
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

VENDOR/COST(where applic.)
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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score greater than or equal to the score of the result being printed
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AAR74919
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AAR72873
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Urea plasminogen a
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Urk t-PA hybrid pep
                                                                                                                                                                                                                             Description
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AAR74920
        Urea plasminogen activator residues 177-184.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR74920;
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                                                                                                                  Negoro T,
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Bifunctional uroki	AAR66245	16	390	100.0	34	45
Human prourokinase	σ	11	389	•	34	44
Bifunctional uroki	AAR66266	16	386	100.0	34	3
[GARSYQ]-[Plasmino	AAR22504	13	380	•	34	42
cPA-P2 Hybrid plas	AAR05433	11	380	•	34	41
Human prourokinase	AAW13635	11	378		34	40
Delta 1-46 urokina	AAR68854	16	365	100.0	34	39
Plasminogen activa	AAR05511	11	349	100.0	34	38 8
n colon	AAG75492	22	337	•	3 •	37
••	AAR99887	17	331		34	
н	AAR99886	17	306		34	
Human prourokinase	AAR10170	12	284	•	34	34
Recombinant scu-PA	AAR25402	13	281	•	34	S S
Recombinant scu-PA	AAR25401	13	281	100.0	34	32
N-terminally modif	AAR47582	15	280	100.0	34	31
N-terminally modif	AAR47581	15	280		34	30
Recombinant scu-PA	AAR25404	13	274		34	29
Recombinant scu-PA	AAR25403	13	274	•	34	28
Recombinant scu-PA	AAR25400	13	274	•	34	27
Recombinant scu-PA	AAR25399	13	274	100.0	ω 4	26
SCU-	AAR25398	13	273	100.0	34	25
Recombinant scu-PA	AAR25397	13	273	100.0	34	24
Recombinant scu-PA	AAR25396	13	272	100.0	34	23
Recombinant scu-PA	AAR25395	13	272	100.0	34	22
Chicken urokinase	AAW27374	18	268	100.0	34	21
	AAR63140	15	259	100.0	ω 4	20
Human urinary type	AAY33122	20	246	100.0	34	19
human	AAY42285	20	246		34	18
Mutant human uroki	AAY39344	20	246		34	17
3	AAG91073	22	232	•	ω 4	16
	AAR64213	16	54		ω 4	15
	AAR64212	16	45		34.	14
	AAR64211	16	39	100.0	u A	3
Urokinase fragment	AAR24949	13	32	100.0	ω A	12

## ALIGNMENTS

Tissue plasminogen activator (t-PA) analogue - has increased fibrin specificity and can be used as an antithrombotic agent. t-PA; tissue plasminogen activator; urea plasminogen activator; UK; variant; fibrin specificity; haemorrhagic tendency. WPI; 1995-155249/20. 01-OCT-1993; 29-JUL-1994; 30-SEP-1994; W09509908-A1 Homo sapiens. (SUMU ) SUMITOMO PHARM CO LTD 13-APR-1995. Sato H; 93JP-0269983. 94JP-0197635. 94WO-JP01629

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AAR74919

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Query Match 100
Best Local Similarity 100
Matches 6; Conservative
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Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 6; Conservative 0; Mismatches 0;
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                                                                                                                                      The urinary plasminogen activator (UK) residues 177-186 are used in a tissue plasminogen activator (t-PA) variant to replace t-PA residues 294-304. The UK replacement region at least contains the sequence of AAR74917. t-PA variants, having residues 280-304 substituted with the corresponding residues from UK, have improved fibrin specificity and are useful in treatment of thrombosis by reducing adverse reactions of
                                                                                             Sequence
                                                                                                                                                                                                                                                   Claim 3; Page 37; 64pp; Japanese.
                                                                                                                                                                                                                                                                                   Tissue plasminogen activator (t-PA) analogue - has increased fibrin specificity and can be used as an antithrombotic agent.
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29-JUL-1994;
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                                                                                                                           haemorrhagic tendency.
                                                                                                                                                                                                                                                                                                                                                                                              (SUMU ) SUMITOMO SEIYAKU KK.
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3 rhrggs 8
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94JP-0197635.
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Pred. No.
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Best Local Similarity
Matches 6; Conserv
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Urokinase; tissue plasminogen activator; PCR; primer; amplification;
thrombosis; blood.
                                             Urokinase
                                                                               06-DEC-1995
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                                                                                                                                         AAR72873 standard; peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tissue plasminogen activator (t-PA) analogue - has increased fibrin specificity and can be used as an antithrombotic agent.
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29-JUL-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                corresponding residues from UK, have are useful in treatment of thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Negoro T,
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(SUMU ) SUMITOMO PHARM CO LTD
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3 rhrggs 8
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                                               fragment from amino acids 177-188.
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                                                                                                                                                                                                                                                                                                                                                                                                             improved fibrin specificity and
s by reducing adverse reactions of
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Best Local Similarity 100.0%;
Matches 6; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Tissue plasminogen activator (t-PA) mutant comprising sequences of urinary plasminogen activator - has improved half life in the blood and may be used to treat thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                 t-PA; tissue plasminogen activator; urea plasminogen activator; variant; fibrin specificity; haemorrhagic tendency.
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                                                                                                                                                                                                                          AAR74927 standard;
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29-JUL-1994;
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                       Negoro T,
                                     (SUMU )
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                                                                                                                                                                        activator residues 163-186.
                                                                                                                                                                                                                          Peptide;
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Pred. No.
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AAR42811
ID AAR4
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tissue plasminogen activator; t-PA; urinary plasminogen activator; u-PA; fibrin; fibrinogen; thrombolysis; thrombus; resistance; plasminogen activation factor inhibiting factor 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The urinary plasminogen activator (UK) residues 163-186 are used in a tissue plasminogen activator (t-PA) variant to replace t-PA residues 280-304. The UK replacement region at least contains the sequence of AAR74917. t-PA variants, having residues 280-304 substituted with the corresponding residues from UK, have improved fibrin specificity and are useful in treatment of thrombosis by reducing adverse reactions of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tissue plasminogen activator (t-PA) analogue - has increased fibrin specificity and can be used as an antithrombotic agent.
                         Tissue plasminogen activator analog improved in fibrin specificity - obtd. by replacing part of aminoacid sequence with corresponding aminoacid sequence of urinary plasminogen activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         u-PA (159-188)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1;
                                                                                                                                                                                                                                                                                                                       Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
Claim 1-6; Page 25-26; 41pp; Japanese
                                                                                                                                                                                  03-APR-1992;
                                                                                                                                                                                                               03-APR-1992;
                                                                                                                                                                                                                                             14-OCT-1993.
                                                                                                                                                                                                                                                                            W09320194-A.
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                                                                                                                     Agui H,
                                                                                                                                                   (SUMU)
                                                                                                                                                                                                                                                                                                                                                      Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       haemorrhagic tendency.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6;
                                                                                                                                                    SUMITOMO PHARM CO LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 53; 64pp;
                                                                                                                     Negoro T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          milarity 100.
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10..20
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19..30
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                                                                                                                     Sato H, Sudo Y,
                                                                                                                                                                                                                                                                                                                                                                                                       "u-PA
                                                                                                                                                                                                                                                                                                                                                                                                                                  "u-PA (159-188); claim 5"
                                                                                                                                                                                                                                                                                                           "u-PA (159-180); claim
                                                                                                                                                                                                                                                                                                                                                                       "u-PA
                                                                                                                                                                                                                                                                                                                                          "u-PA
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ₹
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                                                                                                                         Takahashi
                                                                                                                                                                                                                                                                                                                                                                                                     claim 4"
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2.3;
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Best Local S
Matches 6
Query Match
Best Local Similarity
                                                                                                                                      Analogues of tissue plasminogen activator (t-PA) have amino acids from position 280-304 replaced by the corresponding sequence of urea plasminogen activator (UK). The UK replacement region at least contains the sequence of ARR74917. CS18 comprises a tPA variant (residues 276-306) where residues 294-304 have been replaced by the corresponding UK sequence. The t-PA variants have improved fibrin specificity and are useful in treatment of thrombosis by reducing adverse reactions of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T-PA analogue has at least part of natural t-PA (276-306) substd. with corresp. amino acid sequence of u-PA (159-188). The analogue hardly causes activation of plasminogen (and hence decomposition of fibrinogen), while in circulation (blood). It activates plasminogen to cause thrombolyis when it reaches the locus of the thrombus where fibrin is present. It has high fibrin, and therefore thrombus specificity and is not expected to cause general bleeding as side effect. It also is resistant to plasminogen activation factor inhibiting factor 1. Therefore, the analogue will
                                                                                                                                                                                                                                                                                                                                                    Tissue plasminogen activator (t\text{-PA}) analogue - has increased fibrin specificity and can be used as an antithrombotic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1993;
29-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         t-PA; tissue plasminogen activator; urea plasminogen activator; UK; variant; fibrin specificity; haemorrhagic tendency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UK t-PA hybrid peptide CS11 residues 276-306.
                                                                                 Sequence
                                                                                                                                                                                                                                                                                                            Example 3; Page 50; 64pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1995-155249/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Negoro T, Sato H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-SEP-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    be a safe thrombolytic agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SUMU ) SUMITOMO SEIYAKU KK.
(SUMU ) SUMITOMO PHARM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-APR-1995
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Local Similarity 100.0%;
hes 6; Conservative (
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94JP-0197635.
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Score 34; DB 16; Pred. No. 2.7;
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Pred. No.
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2.7;
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                                                                                                                                                      Query Match 100.0%; Score 34; D
Best Local Similarity 100.0%; Pred. No. 2.
Matches 6; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                Analogues of tissue plasminogen activator (t-PA) have amino acids from position 280-304 replaced by the corresponding sequence of urea plasminogen activator (UK). The UK replacement region at least contains the sequence of AAR74917. CS18 comprises a tPA variant (residues 276-306) where residues 294-302 have been replaced by the corresponding UK sequence. The t-PA variants have improved fibrin specificity and are useful in treatment of thrombosis by reducing adverse reactions of
  13-MAY-1996
                         AAR76947;
                                                                                                                                                                                                                                                                                                                                                                  Tissue plasminogen activator (t-PA) analogue - has increased fibrin specificity and can be used as an antithrombotic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SOMO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UK t-PA hybrid peptide CS14 residues 276-306
                                              AAR76947 standard; Peptide;
                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                             Example 4; Page 50; 64pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1995-155249/20
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29-JUL-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      t-PA; tissue plasminogen activator; urea plasminogen activator;
variant; fibrin specificity; haemorrhagic tendency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-MAY-1996
                                                                                                                                                                                                                                        haemorrhagic tendency.
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                                                                                                         21 rhrggs 26
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| 21 rhrggs 26
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SUMITOMO PHARM CO LTD
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(first entry)
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94JP-0197635
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                                                                                                                                                                              DB 16;
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                                                                                                                                                                              Length 30;
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UK t-PA hybrid peptide CS16 residues

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Query Match
Best Local Similarity
Matches 6; Conser
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29-JUL-1994;
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                                                                                                                                                                                                                                                                                                                                                                                           Analogues of tissue plasminogen activator (t-PA) have amino acids from position 280-304 replaced by the corresponding sequence of urea position activator (UK). The UK replacement region at least contains the sequence of AAR74917 CS15 comprises a tPA variant (residues 276-306) where residues 290-302 have been replaced by the corresponding UK sequence. The t-PA variants have improved fibrin specificity and are useful in treatment of thrombosis by reducing adverse reactions of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tissue plasminogen activator (t-PA) analogue - has increased specificity and can be used as an antithrombotic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Negoro
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                    16-JUL-1993;
                                                                                JP07075580-A
                                                                                                   Synthetic.
                                                                                                                        Urokinase; tissue plasminogen activator; PCR; primer; amplification; thrombosis; blood.
                                                                                                                                                      Urokinase
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                                                                                                                                                                                                                AAR72872 standard;
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                                                                                                                                                                                                                                                                                                                                                                                   haemorrhagic tendency.
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(SUMU ) SUMITOMO SEIYAKU KK
                                       28-DEC-1993;
                                                             20-MAR-1995.
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                                                                                                                                                      peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 51; 64pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sato H;
                                                                                                                                                                                                                                                                                                                                                               30 AA;
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                                                                                                                                                                          (first entry)
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94JP-0197635.
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                    93JP-0199101.
                                        93JP-0354355
                                                                                                                                                      fragment from amino acids 159-188
                                                                                                                                                                                                                  peptide;
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                                                                                                                                                                                                                                                                                                                       Score 34;
Pred. No.
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2.7;
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Query Match
Best Local S
Matches 6
                                                                                                                                                                                                  The peptides AAR72872-3 covering the amino acids (AA) 159-188 or 177-188 of urokinase (UK) were used to replace AA 276-306 of tissue plasminogen activator (t-PA)(AAR72874). The modified t-PA also has several N-Dound sugar chain and additional consensus sequences replaced with urokinase sequences. The replacement was engineered by PCR using the primers AAQ86925-6 to replace the sequences encoding the AA 276-306 in the t-PA cDNA sequence. The modified t-PA may be used in the treatment of thrombosis and has an improved half-life in the blood.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tissue plasminogen activator (t-PA) mutant comprising sequences of urinary plasminogen activator - has improved half life in the blood and may be used to treat thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 2; 13pp; Japanese.
                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1995-151486/20.
1 RHRGGS 6
                                           6; Conserv
                                           100.
nilarity 100.
Conservative
                                                                                                                                                                 30 AA;
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                                                   0
                                                   Score 34; DB
Pred. No. 2.7
0; Mismatches
                                                                       DB
2.7;
                                                                                              16;
                                                   0
                                                                                              Length 30;
                                                     Indels
                                                   0
                                                     Gaps
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AAR71666; Modified urinary plasminogen activator residues 159-188 13-NOV-1995 AAR71666 standard; peptide; 11 (first entry) 30

21 rhrggs

26

Homo sapiens

thrombosis;

Modified urinary plasminogen activator; residues 159-188; tissue plasminogen activator; high fibrin specificity;

systemic bleeding.

JP07039374-A

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10-FEB-1995

28-JUL-1993;

93JP-0207308

93JP-0207308

28-JUL-1993; (SUMU ) SUMITOMO SEIYAKU KK

WPI; 1995-117856/16.

Novel modified tissue plasminogen activator - plasminogen activator peptide fragment contains a urinary

Claim 1; Page 8; 10pp; Japanese

t-PAs can be used bleeding. AAR79104 is the wild type plasminogen activator (t-PA), residues 276-306. By replacing these residues with the uninary plasminogen activator (UK) sequences described in AAR71662-R71666, the fibrinogen specificity of t-PA is increased. The modified t-PAs can be used in the treatment of thrombosis and low systemic

Sequence 30 ξ

Query Match

100.0%; Score 34; B 16; Length 30;

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AAR64211
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Matches 6; Conserv
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Matches
                                                                                                                                                                                                                   The urokinase sequence was used in a contruct for a novel tissue plasminogen activator (tph) having amino acids 276-306 of tph substituted by this urokinase sequence. The tph analogue has resistance to inhibition by plasminogen activator inhibitor (PAI) while retaining its tph activity. The analogue can be used in a drug for the treatment of thrombosis.
       t-PA; tissue plasminogen activator; urinary plasminogen activator; variant; fibrin specificity; haemorrhagic tendency.
                                Urinary plasminogen activator residues 150-188
                                                 13-MAY-1996
                                                                                 AAR64211 standard;
                                                                                                                                                                                                                                                                             Claim 1; Fig 6; 13pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Urokinase fragment
                                                                  AAR64211;
                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                05-OCT-1990;
                                                                                                                                                                                                                                                                                                                                                                                 05-OCT-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                 JP04144682-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR24949;
                                                                                                                                                                                                                                                                                            New tissue plasminogen activator analogue - is resistant inhibitor but retains properties of natural t-PA
                                                                                                                                                                                                                                                                                                                       N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                 19-MAY-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tissue plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR24949 standard;
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                                                                                                                           21 rhrggs 26
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DB; AAQ25737.
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6; Conservative
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ilarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide;
                                                                                 Peptide;
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                                                                                 39 AA
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                                                                                                                                                                  Score 34;
Pred. No.
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                                                                                                                                                            Mismatches
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2.9;
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The urinary plasminogen activator (UR) residues 150-188 are used in a tissue plasminogen activator (t-PA) variant to replace t-PA residues 266-306. t-PA variants, having residues 276-306 substituted with the corresponding residues from UK. have improved fibrin specificity. They are useful in reducing adverse reactions of hemorrhagic tendency. Residues 266-275 and/or 307-321 are opt. substd..
Claim 4; Page 9; 15pp; Japanese. .
                             Novel t-PA variant containing urinary plasminogen activator residues - has improved fibrin specificity to reduce adverse reaction of haemorrhagic tendency
                                                                                                                                                                                                                                                            JP06327473-A.
                                                                                                                                                                                                                                                                                                                          t-PA; tissue plasminogen activator; urinary plasminogen activator; UK; variant; fibrin specificity; haemorrhagic tendency.
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                                                                                                WPI; 1995-047896/07.
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                                                                                                                              (SUMU ) SUMITOMO SEIYAKU KK.
                                                                                                                                                               19-MAY-1993;
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The urinary plasminogen activator (UK) residues 159-203 are used in

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RESULT 15
AAR64213
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Best Local Similarity 100.0%;
Matches 6; Conservative 0
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                                                                                                                                                                                                  The urinary plasminogen activator (UK) residues 150-203 are used in a tissue plasminogen activator (t-PA) variant to replace t-PA residues 266-321. t-PA variants, having residues 276-306 substituted with the corresponding residues from UK, have improved fibrin specificity. They are useful in reducing adverse reactions of haemorrhagic tendency. Residues 266-275 and/or 307-321 are opt. substd..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      t-PA; tissue plasminogen activator; urinary plasminogen activator; UK;
variant; fibrin specificity; haemorrhagic tendency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Urinary plasminogen activator residues 150-203.
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                                                                                                                                                                                                                                                                                                                                                                   Novel t-PA variant containing urinary plasminogen activator residues - has improved fibrin specificity to reduce adverse reaction of haemorrhagic tendency
                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1995-047896/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-MAY-1993;
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                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                Claim 5; Page 9; 15pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SUMU ) SUMITOMO SEIYAKU KK.
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||||||
21 rhrggs 26
1 RHRGGS 6
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30 rhrggs 35
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milarity 100.0%;
Conservative 0,
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                                                                         Score 34; DB 16; Length 54; Pred. No. 4.9; ; Mismatches 0; Indels
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Search completed: March 18, 2002, 09:48:55 Job time: 364 sec

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Result
No.
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Listing first 45 summaries
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Perfect score:
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
   US-09-544-665-1
34
1 RHRGGS 6
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Gapop 10.0 , Gapext 0.
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/cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
/cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
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US-08-560-098A-45
US-08-560-098A-45
US-08-560-098A-45
US-08-560-098A-45
US-08-560-098A-44
US-08-967-024C-25
US-08-153-799-18
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US-09-181-816-1
US-09-181-816-1
US-08-967-8098A-47
US-08-567-8098-47
US-08-568-135-3
US-08-272-255-14
US-08-97-955-905A-22
US-07-955-905A-22
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Sequence 73, Appl
Sequence 45, Appl
Sequence 46, Appl
Sequence 83, Appl
Sequence 83, Appl
Sequence 44, Appl
Sequence 24, Appl
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Sequence 11, Appl
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18, Appl
18, Appl
48, Appl
   Query Match
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RESULT  US-07-942-157A- Sequence 1, A Patent No. 56 GRERAL INFO ADDRESSE STREET: COMPUTER R COMPUTER R MEDIUM T COMPUTER APPLICANT: CIP: 30 COMPUTER APPLICANT COMPUTER APPLICANT FILING D CLASSIFI FRIOR APPLICAT APPLICAT APPLICAT FILING D CLASSIFI FRIOR APPLICAT FILING D CLASSIFI FRIOR APPLICAT APPLI	4444433333333228 544444339553333333333333333333333333333
57A-1 1, Application . 5648253 ANT: Wei; Cha- OF INVENTION: OF SEQUENCES: ESSEE: Kilpatt ET: 1100 Peach ER READBREE FOODERES ASTYPE: Floop UM TYPE: Floop UTER: IEM PC ATING SYSTEM: WARE: PAtentin TAPPLICATION UMBER: NG DATE: 1920 SIFICATION NUMBER: NG DATE: 1920 TOTATION DATE: PANION DATE: PHONE: (404)815- TON FOR SEQ ID CE CHARACTERIST TH: 6 AMINO ACID DE CHARACTERIST THE MINO ACID NEW TYPE: WEITH NO NO TYPE: NO NT T	30 888.2 30 888.2 30 888.2 30 888.2 30 888.2 30 888.2 30 888.2 30 888.2 30 888.2 30 888.2 31 32 32 32 32 32 32 32 32 32 32 32 32 32
US/07942157# Mer Inhibitor-Re 3 3 1 Ck & Cody tree Street	323 1 US-08-0 336 2 US-08-2 336 2 US-08-9 337 3 US-08-9 237 2 US-08-7 237 2 US-08-7 237 4 US-08-7 237 4 US-08-8 4 US-08-8 4 US-08-8 1124 5 PCT-US-9 1125 2 US-08-7 1125 3 US-08-8 1125 3 US-08-8 1125 3 US-08-8 1125 3 US-08-8 1126 3 US-08-8 1127 3 US-08-8 1128 3 US-08-8 1129 3 US-08-8 1121 3 US-08-8 1121 3 US-08-8 1122 3 US-08-8 1123 3 US-08-8
suite 2800 Suite 2800 Suite 273 0, Version #1.25 157A	08-026-138E-4 08-486-273A-58 08-486-273A-58 08-940-086A-58 08-425-543A-48 08-723-305C-48 09-425-007-2 08-425-007-2 08-425-007-2 08-417-87-2 08-417-87-2 08-418-16 08-891-848-16 08-891-848-16 08-891-848-16 08-891-848-16 08-891-848-16 08-891-848-16 08-891-848-16 08-891-848-16
	Sequence 4, Appl. Sequence 58, App. Sequence 58, App. Sequence 48, App. Sequence 48, App. Sequence 47, App. Sequence 47, App. Sequence 47, App. Sequence 22, Appl. Sequence 5, Appl. Sequence 5, Appl. Sequence 11, App.

100.0%;

Score 34; DB 1;

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RESULT 3
US-08-560-098A-49
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                                                                                                                                                         Ouery Match 100.0%; Score 34; DB 4; Length 253; Best Local Similarity 100.0%; Pred. No. 17; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.0%; Pred. No. 1.6e+05; Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                  NFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6232456e
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Becker Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183.US.01
ELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
TORNEY/AGENT INFORMATION:
                                                                                                       1 RHRGGS 6
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                                                                                 RHRGGS 26
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100 Abbott Park Road
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GRANADOS, EDWARD N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COHEN, MAURICE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOVEL SERINE PROTEASE REAGENTS AND METHODS USEFUL FOR DETECTIOF THE PROSTATE
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Best Local Similarity 100.
Conservative
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                                                                                                                                                                                                                                                                                                                                                        -08-560-098A-45
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PRICH APPLICATION DATA:
17-NOV-1995
PRICH APPLICATION DATA:
APPLICATION NUMBER: P 44 40 8
FILING DATE: 17-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 148/
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                       equence 45,
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NFORMATION FOR SEQ ID NO.
                                                                                                                                                                                                                                                                                  Lent No. 59,000.
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APPLICANT: HEINZEL-WIELAND, Regina
APPLICANT: STEFFENS, Gerd Josef
TITLE OF INVENTION: Proteins having Fibrinolytic and
TITLE OF INVENTION: Coagulation-inhibiting Properties
NUMBER OF SEQUENCES: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
TYPE: amino acid
STRANDEDURESS: Single
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CURRENT APPLICATION DATA:
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                                                                                                                                                                      APPLICANT: WNENDT, Stephan
APPLICANT: HEINZEL-WIELAND, Regina
APPLICANT: STEFFENS, Gerd Josef
TITLE OF INVENTION: Proteins having Fibrinolytic and
TITLE OF INVENTION: Coagulation-inhibiting Properties
NUMBER OF SEQUENCES: 60
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                         CORRESPONDENCE ADDRESS:
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                                       STATE: DC
COUNTRY: US
ZIP: 20005
                                                                                            ADDRESSEE: Evenson, McKeown, Edwards & Lenahan STREET: 1200 G Street, N.W., Suite 700 CTITE: Mashington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Pred. No.
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Matches
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MEDIUM TYPE: Floppy of COMPUTER: IBM PC comp
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                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                        APPLICATION NUMBER: US/08/560,0981
FILING DATE: 17-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P 44 40 892.7
FILING DATE: 17-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 146
TELECOMMUNICATION INFORMATION:
TELEPHONE: / 2020.
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FILING DATE: 17.NOV-1995
PRIOR APPLICATION DATA: 44 0 892.7
APPLICATION NUMBER: P 44 40 892.7
FILING DATE: 17.NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 14-
TELECOMMUNICATION INFORMATION:
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CITY: Washington
STATE: DC
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REGISTRATION NUMBER: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                               LE OF INVENTION: Proteins having Fibrinolytic and Coagulation-inhibiting Properties
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5976841
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1200 G Street, N.W., Suite 700
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ilarity 100.0%;
Conservative 0
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HEINZEL-WIELAND,
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                       148/42448
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Best Local Similarity
Matches 6; Conserve
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                                                                                                                                              INFORMATION FOR SEG ID NO: 83
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PATIOR APPLICATION NUMBER: DE P43 23 754.1
PILING DATE: 15-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: (202)628-8800
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74 RHRGGS 79
133 RHRGGS 138
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TYPE: a
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                                                                      Local
                                                                                                                                                                                                                                                                     NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 14
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                         1 RHRGGS 6
                                                       similarity
6; Conserv
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1200 G Street, N. W. Suite 700
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                                                                                                                                                                                                          (202)628-8844 `
DR SEQ ID NO: 83:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EINZEL-WIELAND, REGINA
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Pred. No. 22;
                                                                         Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Version #1.25
                                                                                       DB 1; Length 365;
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Query Match
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US-08-720-012-83
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FILING DATE: 20-JUL-1993
APPLICATION NUMBER: DE P43 23 754.1
FILING DATE: 15-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, JOSEPh D.
REGISTRATION NUMBER: 26,269
REGISTRATION NUMBER: 26,269
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/01
FILING DATE: 27-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FITLE OF INVENTION: FITLE OF INVENTION:
                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                133 RHRGGS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (202)628-8800
                                               ITLE OF INVENTION: ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Polonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
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                                                                                                                                                                                                                                                                                1 RHRGGS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
              DDRESSEE:
                                                                                                                                                                  44, Application US/08560098A
o. 5976841
                                                                                                                                               INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSEE: Evenson, McKeown, Edwards & Lenahan
T: 1200 G Street, N. W. Suite 700
Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/08720012
E: Evenson, McKeown, Edwards & Lenahan 1200 G Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                               365 amino acids
                                                                                               STEFFENS, Gerd Jose:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (202)628-8844
OR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WNENDT, STEPHAN
SCHNEIDER, JOHANNES
HEINZEL-WIELAND, REGINA
SAUNDERS, DEREK J
                                                                                                              HEINZEL-WIELAND, Regina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STEFFENS, GERD J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
                                              Proteins having Fibrinolytic and Coagulation-inhibiting Properties: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INHIBITING EFFECT
83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BIFUNCTIONAL UROKINASE VARIANTS WITH IMPROVED FIBRINOLYTIC CHARACTERISTICS AND THROMBIN
                                                                                                                                                                                                                                                                                                                                             100.0%; Score 34; DE 100.0%; Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Release #1.0, Version #1.25
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                                                              Properties
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Best Local :
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TELEFAX: (202) 628-880 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS PRIOR APPLICATION DATA:
APPLICATION NUMBER: P 44 40 892.7
APPLICATION NUMBER: P 744 40 892.7
APPLICATION NUMBER: P 750V-1994 TELECOMMUNICATION INFORMATION: CURRENT APPLICATION DATA: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0 NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 26
REFERENCE/DOCKET NUMBER: STRANDEDNESS APPLICATION NUMBER: US/U amino acid TYPE: (202) linear (202) 628-8844 628-8800 Release #1.0, Version #1.30 (EPO) US/08/560,098A 148/42448

1 RHRGGS 6 Local Similarity es 6; Conserv Conservative 100.0%; 0 Score 34; Pred. No. DB 2; Length 393; 0 Gaps

0,

APPLICANT: WNEARCH, Gerd APPLICANT: STEFFENS, Gerd APPLICANT: JANCCHA, Elke APPLICANT: HEINZEL-WIELANT Chime ENERAL INFORMATION: COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA: PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 30-NOV-CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N.W., Sulte 700 ATTORNEY/AGENT INFORMATION: TILE OF INVENTION: Chimeric Proteins having Fibrinolytic CLASSIFICATION: 435 FILING DATE: APPLICATION NUMBER: 24, Application US/08967024C o. 6133011 Washington Patentin Release #1.0, Version #1.30 (EPO) Stephan Gerd Josef US/08/967,024C 42 665.8

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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-967-024C-24
                                                                                                              ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-967-024C-25
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                  Query Match
Best Local Similarity
6; Conserv
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                  NFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P 44 42 665.8
FILING DATE: 30-NOV-1994
ATTORNEY/AGENT INFORMATION:
AND TOOLS TOOLS TOOLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible operating system: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: LC
STATE: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 RHRGGS 139
                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 14
ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORRESPONDENCE ADDRESS:
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                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 393 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPLICANT: STEFFENS, Gerd Josef
PPLICANT: JANOCHA, EIKe
PPLICANT: HEINZEL-WIELAND, Regina
ITLE OF INVENTION: Chimeric Proteins having Fibrinolytic
UMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RHRGGS 6
                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                  NAME: EVANS, JOSEPH D. REGISTRATION NUMBER: 2
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1 RHRGGS 6
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amino acid
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                               100.0%; ilarity 100.0%; Conservative 0
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                                                               DB 4; Length 393;
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                               Indels
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US-08-286-748B-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SENERAL INFORMATION:
                                                                                APPLICANT: Victor Gui
TITLE OF INVENTION: (
TITLE OF INVENTION: (
TITLE OF INVENTION: (
NUMBER OF SEQUENCES:
                                                                                                                                                                                     tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: UPPER DESCRIPTION NUMBER: UPPER DESCRIPTION: 514 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: WordPerfect (Version 5.1) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Diskette,
                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,9
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
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les 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE:
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                                                                                                                                                                                                                                                                                                                    1 RHRGGS 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E OF INVENTION:
                                                                                                                                                                                   18, Application US/08286748B
o. 5759542
                                                                                                                                                                    INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , Application US/08087163 5472692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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   Massachusetts
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ilarity 100.0%;
Conservative 0
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                                                                                                                                                   Victor Gurewich
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SYSTEM: MS-DOS (Version 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fish & Richardson
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ich, Victor
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                                                                                                                 COMPOSITIONS AND METHODS FOR THE DELIVERY OF DRUGS BY PLATELETS FOR THE TREATMENT OF
                                                                                                 CARDIOVASCULAR AND OTHER DISEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US/08/087,163
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                                                                                                                                                                                                                                                                                                                                                                        Score 34;
Pred. No.
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Indels

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TREATMENT OF

26-APR-1990

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RESULT 13
US-08-153-799-18
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: J. Peter Fasse
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 0454
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5570
TELEFAX: (617) 542-8906
                                                                                                                                            COMPUTER READABLE FORN:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS_MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/153,799
FILING DATE:
                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847975
FILING DATE: 06-MAR-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: August 5, 1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PS/2 Model 502 or 558X OPERATING SYSTEM: MS-DOS (Version 5.0) SOFTWARE: Wordperfect (Version 5.1) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 RHRGGS 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" D1
                                                                                                                                                                                                                                                                                                                                                                                                              PPLICANT: Goodey, Andrew R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: Augus
                                                                                                                                                                                                                                                                                                            ADDRESSEE: R Hain Swope, BOC Health Care Inc
STREET: 100 Mountain Avenue
CITY: Murray Hill
STATE: New Jersey
RIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB90/00650
                                   APPLICATION NUMBER: FILING DATE: 29-AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                  COUNTRY: U
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02110-2804
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ilarity 100.0%;
Conservative 0
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linear
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                                 29-APR-1989
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                                                 GB 8909916.2
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Pred. No. 27;
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   MOLECULE TYPE:
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                                                                ENGTH:
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REPLICATION UNBER: US 07/775952

APPLICATION NUMBER: US 07/775952

FILING DATE: 29-OCT-1991

ANTORNEY, AGENT INFORMATION:

NAME: SWODE, R Hain
REGISTRATION NUMBER: 24864

REFERENCE/DOCKET NUMBER: 928832

TELECOMMUNICATION 1NFORMATION:

TELEPHONE: (908) 665 2400

TELERAX: (908) 771 6159

TELEPHONE: (908) 771 6159

TELEPHONE: SWOD ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 411 amino acids

TYPE: amino acids

TYPE: amino acid

TYPE: amino acid

TYPE: amino acid

TYPE: maino acid

TYPE: maino acid

TYPE: protein

US-08-153-799-18

Ouery Match
Best Local Similarity 100.0%; Score 34; DB 1; Length 411;
Best Local Similarity 100.0%; Pred. No. 27;

Matches 6; Conservative 0; Mismatches 0; Gaps

Oy 1 RHRGS 6

179 RHRGS 6

179 RHRGS 184
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TELEFAX: (202) 628-8844 INFORMATION FOR SEQ ID NO: 48: FILING DATE: 17-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D.
REGISTRATION NUMBER: 26, APPLICATION NUMBER: US/08/560,098/ FILING DATE: 17-NOV-1995 PRIOR APPLICATION DATA: APPLICATION NUMBER: P 44 40 892.7 FILING DATE: 17-NOV-1994 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA: ENERAL INFORMATION: REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION
TELEPHONE: (202) 628-8800 SEQUENCE CHARACTERISTICS: CORRESPONDENCE ADDRESS: APPLICANT: HEINZEL-WIELAND, Regina
APPLICANT: STEFENS, Gerd Josef
TITLE OF INVENTION: Proteins having Fibrinolytic and
TITLE OF INVENTION: Coagulation-inhibiting Properties 179 RHRGGS 184 UMBER OF SEQUENCES: STREET: 1200 G S CITY: Washington STATE: DC TYPE: amino acid STRANDEDNESS: single Application US/08560098A 411 amino acids E: Evenson, McKeown, Edwards & Lenahan 1200 G Street, N.W., Suite 700 WNENDT, Stephan HEINZEL-WIELAND, Regina USA linear US/08/560,098A 26,269 148/42448

protein

US-08-560-098A-48

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Query Match
Best Local Similarity 100.0%; Score 34; DB 2; Length 411;
Best Local Similarity 100.0%; Pred. No. 27;

QY 1 RHRGS 6
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Db 179 RHRGS 184

RESULT 15
| US-09-181-816-1
| Sequence 1, Application US/09181816
| Patent No. 6277816
| Patent No. 6277816
| Patent No. 6277817
| Patent No. 6277817
| APPLICANT: MAZAR, Andrew P.
APPLICANT: JONES, Terence R.
APPLICANT: JONES, Terence R.
ITILE OF INVENTION: CYCLIC PEPTIDE LIGANDS THAT TARGET UROKINASE
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Maximum DB seq length: 2000000000
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     A;Molecule type: mRNA
A;Residues: 1-150,'w',152-213,'I',215-385,'C',387-429,'V',431 <JAC>
A;Cross-references: EMBL:X02760; NID:g35297; PIDN:CAA26535.1; PID:g35298
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		ribosomal protein	probable transcrip	ribosomal protein	L2 ribosomal prote	probable L2 riboso	ribosomal protein								

## ALIGNMENTS

Proc. Natl. Acad. Sci. U.S.A. 81, 4727-4731, 1984 A;Title: Identification and primary sequence of an unspliced human urokinase poly(A) A;Reference number: A37561; MUID:84272706 A;Accession: A37561 A;Molecule type: mRNA A;Residues: 66-431 <ver> A;Cross-references: GB:D00244; NID:g220138 A;Cross-references: GB:D00244; NID:g220138 A;Cross-reference GB:D00244; NID:g220138 A;Title: Molecular cloning, sequencing, and expression in Escherichia coli of human: A;Reference number: I38102; MUID:85203359 A;Accession: I38102 A;Status: preliminary</ver>	A; Molecule type: DNA A; Residues: 145-161 < NAGI> A; Cross-references: GB: K03027; NID:g340174; PIDN:AAA61257.1; PID:g340175 A; Roterence number: JT0102; MUID:86056954 A; Accession: JT0102 A; MOlecule type: mRNA A; Cross-references: GB: K03226; NID:g340155; PIDN:AAC97138.1; PID:g340158; GB:D00244; A; Cross-references: GB: K03226; NID:g340155; PIDN:AAC97138.1; PID:g340158; GB:D00244; A; Verde, P.; Stoppelli, M.P.; Galeffil, P.; Dl Nocera, P.; Blasi, F.	A;Title: The human urokinase plasminogen activator gene and its promoter. A;Reference number: A00931; MUID:85215647 A;Reference number: A00931 A;Molecule type: DNA A;Residues: 1-431 <ric> A;Cross-references: GB:X02419; NID:g37601; PIDN:CAA26268.1; PID:g1834524 A;Cross-references: GB:X02419; NID:g37601; PIDN:CAA26268.1; PID:g1834524 A;Cross-references: Cammun. However the authors translated the codon ATG for residue 214 as Ile R;Nagamine, Y:, Pearson, D.; Grattan, M. R;Nitle: Exon-intron boundary sliding in the generation of two mRNAs coding for porc A;Reference number: I52209; MUID:86050639 A;Accession: I52209; Translated from GB/EMBL/DDBJ A;Status: preliminary; translated from GB/EMBL/DDBJ</ric>	RESULT 1  UKHU  UKHU  URHU  UPLASMINOGEN activator (EC 3.4.21.73) precursor [validated] - human  N;Alternate names: cellular plasminogen activator; urokinase; urokinase-type plasminogen  N;Contains: urokinase-type plasminogen activator chain A; urokinase-type plasminogen  in form  C;Species: Homo sapiens (man)  C;Date: 17-Dec-1982 #sequence_revision 04-Dec-1986 #text_change 15-Sep-2000  C;Accession: A00931; 152209; JT0102; A37561; 138102; S65783; A37562; A37564;  R;Riccio, A,; Grimaidi, G.; Verde, P.; Sebastio, G.; Boast, S.; Blasi, F.  Nucleic Acids Res. 13, 2759-2771, 1985

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A;Gene: GDB:PLAU
A;Cross-references: G
A;Map position: 10g24
A;Introns: 19/3; 29/1
C;Function: proteo
A;Description: proteo
A;Pathway: fibrinolys
C;Superfamily: urokin
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A;Molecule type: protein
A;Molecule type: protein
A;Residues: 21-30,'X',32',X',34-38,'X',40-43 <KEN>
A;Residues: 21-30,'X',32,'X',34-38,'X',40-43 <KEN>
A;Residues: 21-30,'X',32,'X',34-38,'X',40-43 <KEN>
A;Note: identification of a fucose and attempt to determine its attachment site
A;Rabbani, S.A.; Desjardins, J.; Bell, A.W.; Banville, D.; Mazar, A.; Henkin, J.
Biochem. Biophys. Res. Commun. 173, 1058-1064, 1990
A;Title: An amino-terminal fragment of urokinase isolated from a prostate cancel
A;Title: An amino-terminal fragment of urokinase isolated from a prostate cancel
                                                                                                                                                                                                                                                                                                               A;Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR R;Hansen, A.P.; Petros, A.M.; Meadows, R.P.; Nettesheim, D.G.; Mazar, A.P.; Olej submitted to the Brookhaven Protein Data Bank, January 1994
A;Reference number: A6682; pdb:1URK
A;Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR, R;Spraggon, G.S.; Phillips, C.; Nomak, U.K.; Ponting, C.P.; Saunders, D.; Dobson submitted to the Brookhaven Protein Data Bank, July 1995
A;Reference number: A66058; Pdb:1LMM
A;Contents: annotation; X-ray crystallography, 2.5 angstroms, residues 168-175;1
C;Comment: Urokinase-type plasminogen activator proteolytically activates plasming.
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A;Molecule type: Protein
A;Residues: 21-34 <RAB>
R;Li, X.; Bokman, A.M.; Llinas, M.; Smith, R.A.G.; Dobson, C.M.
R;Li, X.; Bokman, A.M.; Llinas, M.; Smith, R.A.G.; Dobson, C.M.
submitted to the Brookhaven Protein Data Bank, July 1993
A;Reference number: A51255; PDB:!KDU
A;Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR,
A;Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR,
B;Ci, X.; Smith, R.A.G.; Dobson, C.M.
Biochemistry 31, 9562-9571, 1992
A;Title: Sequential (1)H NMR assignments and secondary structure of the kringle d
A;Reference number: A44375; MUID:93003110
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A:Residues: 156-176;179-193,'T',195,'T',197-224 <SCH>
A:Residues: 156-176;179-193,'T',195,'T',197-224 <SCH>
R:Steffens: G.J.; Gunzler, W.A.; Otting, F.; Frankus, E.; Flohe, L.
Hoppe-Seyler's Z. Physiol. Chem. 363, 1043-1058, 1982
Hoppe-Seyler's Z. Physiol. Chem. 363, 1043-1058, 1982
A:Title: The complete amino acid sequence of low molecular mass urokinase
A:Reference number: A37564; MUID:B3055099
A:Accession: A37564
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A;Residues: 21-17 <GUN>
R;Schaller, J; Nick, H; Rickli, E.E.; Gillessen, D.;
R;Schaller, J; Nick, H; Rickli, E.E.; Gillessen, D.;
Eur. J. Biochem. 125, 251-257, 1982
A;Title: Human low-molecular weight urinary urokinase.
A;Reference number: A37563; MUID:83003608
A;Accession: A37563
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A;Title: Characterization of single chain urokinase-type plasminogen activator with a A;Reference number: S65783; MUID:96186279
A;Accession: S65783
                                                                        Description: proteolytically activates plasminogen
                                                                                                                                                                                                                                                                                               Genetics:
                                        fibrinolysis
urokinase-type plasminogen activator; EGF
                                                                                                                                                                                                                  GDB:119497; OMIM:191840
                                                                                                                                             154/1; 227/2;
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igh molecular mass form, consisting of a
proteolytically activates plasminogen,
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Matches 6
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les 6; Conserv
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A; Molecule type: mRNA
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A;Title: Bovine urokinase-type plasminogen A;Reference number: JN0560; MUID:93216119
A;Accession: JN0560
                                                                                                                                                                                                   u-plasminogen activator (EC 3.4.21.73) precursor - bovine N;Alternate names: upA C;Species: Bos primigenius taurus (cattle) C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_C;Accession: JN0560
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ision 31-Dec-1993 #text_change 16-Jul-1999
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Pred. No. 15;
0; Mismatches C
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                                                                                                                                                                   S.; Rifkin, D.B.; Schleuning, W.D.
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adenosylhomocysteinase (EC 3.3.1.1) DKF2p564A1523 - N;Alternate names: protein DKF2p564A1523.1 C;Species: Homo saniene /m---
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Superfamily: urokinase-type plasminogen activator; EGF homology; kringle homology; try
;Keywords: glycoprotein; heterodimer: hydrolase; kringle; serine proteinase
;1-20/Domain: signal sequence *status predicted <SIG>
21-188/Product: urokinase-type plasminogen activator chain A *status predicted <ACH>
;33-64/Domain: EGF homology <CGF>
;72-153/Domain: EGF homology <CGF>
;72-153/Domain: kringle homology <KRG>
;190-442/Product: urokinase-type plasminogen activator chain B *status predicted <BCH>
;190-430/Domain: trypsin homology <TRY>
;190-440/Domain: trypsin homology <TRY>
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Date: 04-Dec-1986 #sequence_revision 17-Mar-1987 #text_change 07-Aug-1998
Accession: A00932
Nagamine, Y.: Pearson, D.: Altus, M.S.: Reich, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ubmitted to the Protein Sequence Database, December 1986 Reference number: A37566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         orleic Acids Res. 12, 9525-9541, 1984
Title: CDNA and gene nucleotide sequence of porcine plasminogen activator
Reference number: A00932; MUID:85087954
Accession: A00932
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Best Local Similarity
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Residues: 1-240, 'H', 242-442 <NAG1>
Experimental source: kidney cell line LLC-PK1
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210 RHRGGS 215
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ilarity 100.0%;
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D; Mismatches
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K; Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, submitted to the Protein Sequence Database, May 1999
A; Reference number: Z16469
A; Accession: T08681
                                            A; NoLecule type: DNA
A; NoLecule type: DNA
A; Residues: 1-1332 <WIL>
A; Residues: 1-1332 <WIL>
A; Cross-references: EMBL: 292789; PIDN: CABO7215.1; GSPDB: GN00022; CESP: H02I12.1
A; Cross-references: clone H02I12
                                                                                                                                                                submitted to the EMBL Data Library, A; Reference number: Z19656 A; Accession: T23024
                                                                                                                                                                                                                                                                hypothetical protein H02I12.1 · Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change
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A; Residues: 1-1217 <G
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R; Garel, A.A.; Dele
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C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Sep-1997
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C;Keywords: NAD; thioether hydrolase
F;379-408/Region: beta-alpha-beta NAD nucleotide-binding
F;244,278/Active site: Cys #status predicted
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C;Accession: T08681
A; Introns: 12/3; 29/1; 60/3; 246/1; 449/1; 756/1; 849/1; 961/1; 1103/3; 1214/3
                                                                                                                                                                                                                             R;McLay,
                                                                                                                                                                                                                                              C; Accession:
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A; Accession: S52714
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A;Residues: 1-597 <WAM>
A;Cross-references: EMBL:AL049954
                                      A;Gene: CESP:H02I12.1
                                                                                                                                              A; Status: preliminary; translated from GB/EMBL/DDBJ
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Matches 6
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Matches 6
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731 RHRGGS 73
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6; Conserv
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nilarity 100.0%;
Conservative 0
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probable C2H2-type zinc finger protein [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 *sequence_revision 02-Feb-2001 *text_change 02-Feb-2001 C;Accession: C84688 F;Lin, X.; Kaul, S.; Roungley C? ~ ~ ~
                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-86 <BEC>
A;Cross-references: GB:L05062; NID:g304570; PIDN:AAA28287.1; PID:g304571
A;Cross-references: venom gland
A;Experimental source: venom gland
C;Superimenty: scorpion neurotoxin
C;Superimenty: scorpion neurotoxin
C;Keywords: toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Becerril, B.; Vazquez, A.; Garcia, C.; Corona, M.; Bolivar, F.; Possani, L.D. Gene 128, 165-171, 1993
A;Title: Cloning and characterization of cDNAs that code for Na+-channel-blocki A;Reference number; JN0669; MUID:93292983
A;Accession: JN0671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Na+-channel-blocking toxin (clone cngtIV) precursor - scorpion (Centruroides noxius) C;Species: Centruroides noxius C;Species: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 16-Jul-1999
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A;Molecule type: protein
A;Residues: 1-64 <POS>
C;Superfamily: scorpion neurotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Possani, L.D.; Martin, B.M.; Svendsen, I.; Rode, G.S
Biochem. J. 229, 739-750, 1985
A;Title: Scorpion toxins from Centruroides noxius and
A;Reference number: 332789; MUID:86025386
A;Accession: 332789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           toxin II-14 - scorpion (Centruroides noxius)
C;Species: Centruroides noxius
C;Species: Chart-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999
C;Accession: S32789
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Best Local Similarity 83.3
Matches 5; Conservative
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86/Product: Na+-channel-blocking toxin (clone cngtIV) *status
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83.3%;
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Pred. No. 15;
1; Mismatches
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    Town, C.D.; Fujii,
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C; Species: Ps
C; Date: 15-Se
C; Accession:
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Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487
A;Accession: C84688
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-156 < STO>
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-310 <YOS>
A;Cross-references: EMBL:D89241; NID:g1749689; PIDN:BAA13902.1; PID:g1749690
A;Experimental source: strain PR745
                                                                                                  R;YOShloka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H. DNA RES. 4; 363-369, 1997
DNA RES. 4; 363-369, 1997
A;Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs A;Reference number: 217323; MUID:98162722
A;Reference number: 217323; MUID:98162722
A;Accession: T43147
                                                                                                                                                                                                               hypothetical protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
C;Accession: T43147
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Nature 406, 959-964, 2000
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C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
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A;Gene: At2g28710
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Matches 5; Conserv
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Best Local Similarity 83.3
Matches 5; Conservative
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A.; Larbig,
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                                                                                                                                                                  Superfamily: toluene dioxygenase terminal oxygenase component large chain; Rieske | Reywords: 2Fe-2S; aromatic hydrocarbon catabolism; metalloprotein; oxidoreductase; Keywords: 2Fe-2S; aromatic hydrocarbon catabolism; metalloprotein; oxidoreductase; 65-113,Domatic Rieske [2Fe-2S] homology <RSK>
(55-713,Domatic Rieske [2Fe-2S] cluster (Cys, His, Cys, His) (covalent) #status pu
                                                                                                                                                                                                                                                                                                                 Cross-references: GB:AF060489
Experimental source: strain CB3
Comment: This protein is the initial dioxygenase large (alpha) subunit in the carbazo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         arbazole dioxygenase (EC 1.14.-.-) terminal oxygenase component large chain carAa -
Species: Sphingomonas sp.
Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 18-Jun-1999
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Superfamily: unassigned ATP-binding cassette proteins; ATP-binding
Keywords: ATP
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Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Tille: Deciphering the biology of Mycobacterium Reference number: A70500; MUID:98295987
Accession: G70800
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Cole, S.T.; Brosci
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Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Title: Novel car
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Shepherd, J.M.;
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hem. Biophys. Res. Commun. 247, 129-135, 1998
tle: Novel carbazole degradation genes of Sphingomonas CB3: Sequence analysis, transference number: JW0098; MUID:98300296
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                                      y Match 91.2%;
Local Similarity 83.3%;
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1; Mismatches
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Pred. No. 47;
1; Mismatches
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C; Superfamily: common tobacco sucrose transport protein
                                                                                                                                                                                                                                                                                      Plant Physiol. 118, 1473-1480, 1998
A;Title: Characterization of source- and sink-specific sucrose/H+ symporters from A;Reference number: Z17991; MUID:99063785
                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-501 <SHA>
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                                                                                                                                                                                                     Experimental source:
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Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
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RA angiogenic protein from bovine serum and milk -- purification and reference protein from bovine serum and milk -- purification and protein from bovine serum and milk -- purification and reference protein from bovine serum and milk -- purification and reference protein from bovine serum and milk -- purification and reference protein from bovine serum and milk -- purification and reference protein from bovine serum and milk -- purification and reference protein from bovine serum and milk -- purification and reference protein from bovine serum and milk -- purification and reference protein from bovine serum and milk -- purification from bovine serum and milk -- purification and reference protein synthesis inhibitor; Glycoprotein from bovine carbovylic accidence protein synthesis inhibitor; Glycoprotein from protein synthesis inhibitor; Glycoprotein from protein synthesis inhibitor; Glycoprotein from bovine carbovylic accidence protein synthesis inhibitor; Glycoprotein from bovine graph of the protein synthesis inhibitor; Glycoprotein from bovine graph and protein synthesis inhibitor; Glycoprotein from bovine graph and protein synthesis inhibitor; Glycoprotein from bovine graph and bovine synthesis from bovine graph and graph a
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Eukaryota; Methazia; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANG2_BOVIN STANDARD; PRT; 123 AA. P80929; O1-KOV-1997 (Rel. 35, Created) O1-KOV-1997 (Rel. 35, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update) NAGIOGENIN-2 (EC 3.1.27.-).
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MEDLINE-85215647; PubMed-2987867;
MEDLINE-85215647; PubMed-2987867;
Riccio A., Grimaldi G., Verde P., Sebastio and The human urokinase-plasminogen activator and the human urokinase. 13:2759-2771(1985).
                                                                                                                                                                                                                                                                                    "The primary structure of high molecular mass urokinase i urine. The complete amino acid sequence of the A chain."; Hoppe-Seyler's Z. Physiol. Chem. 363:1155-1165(1982).
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                                                                                             MEDIINE-83055099; PubMed-6754572;
Steffens G.J., Gunzler W.A., Otting F., Frankus E., Flohe L.;
"The complete amino acid sequence of low molecular mass urokinase from human urine.";
                                                                                                                                                                                                 "Human low-molecular-weight urinary urokinase. characterization and preliminary sequence data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nagai M., Hiramatsu R., Kaneda T.,
Nishida M., Suyama T.;
"Molecular cloning of cDNA coding
Gene 36:183-188(1985).
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20-MAR-1987 (Rel. 04, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
UROKINASE-TYPE PLASMINGCEN ACTIVATOR PRECURSOR (EC 3.4.21.73) (UPA)
MEDLINE-96000858; PubMed-8591045;
Spraggon G., Phillips C., Nowak U.K., Ponting C.P., Saunders
Dobson C.M., Stuart D.I., Jones E.Y.;
"The crystal structure of the catalytic domain of human
                                                                                                                                                                Eur. J. Biochem. 125:251-257(1982)
[7]
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Schaller J., Nick H., Rickli E.E., Gillessen D., Lergier
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Verde P., Stoppelli M.P., Galeffi P.,
"Identification and primary sequence
poly(A)+ RNA.";
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Nagai M., Hiramatsu R., Kaneda T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Holmes W.E., Pennica D., Blaber M., Rey
Steffens G.J., Heyneker H.L.;
"Cloning and expression of the gene for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
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Mammalia; Eutheria; Primates;
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.55084; PubMed-6754569;
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RY MEDLINE-97337920; PubMed-9194591;
RA Turkmen B., Schmätt M., Schmälfeldt B., Trommler P., Hell W.,

RA Turkmen B., Schmätt M., Schmälfeldt B., Trommler P., Hell W.,

RA Turkmen B., Schmätt M., Magdolen V.;

RA Creutzburg S., Graeff H., Magdolen V.;

RA Creutzburg S., Graeff H., Magdolen V.;

RA Electrophoresis 18:686-689(1997).

RE Electrophoresis 18:686-689(1997).

RE Electrophoresis 18:686-689(1997).

RE ELECTROPHORE PLASHINOGEN ACTIVATOR AND IS CLINICALLY USED FOR THERAPY OF THROMBOLYTIC DISORDERS.

C. -- FUNCTION: POTENT PLASHINOGEN ACTIVATOR AND IS CLINICALLY USED FOR C.

C. -- CATALYTIC ACTIVITY: SPECIFIC CLEAVAGE OF ARG-|-VAL BOND IN C.

C. -- CATALYTIC CATIVITY: SPECIFIC CLEAVAGE OF ARG-|-VAL BOND IN THE HIGH MOLECULAR MASS FORM CONTAINS A CC PLASHINOGEN TO FORM PLASHIN.

C. -- SUBUNIT: FOUND IN HIGH AND LOW MOLECULAR MASS FORM CONTAINS A LONG CHAIN A. CLEAVAGE OCCURS AFTER RESIDUE 155 IN THE LOW MOLECULAR MASS FORM TO YIELD A SHORT A1 CHAIN.

C. -- SUBULLARITY: CONTAINS 1 EGF-LIKE DOMAIN.

C. -- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

C. -- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT LEU-141.
MEDLINE-9721855; PubMed-9065988;
Conne B., Berczy M., Belin D.;
Detection of polymorphisms in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Li X., Bokman A.M., Llinas M., Smit
"Solution structure of the kringle
plasminogen activator.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature
[10]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-89127526; PubMed-2536903;
Oswald R.E., Bogusky M.J., Bamberger M., Smith R.A.G., Dobson C.M "Dynamics of the multidomain fibrinolytic protein urokinase from dimensional NMR.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conne B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yoshimoto M., Ushiyama Y., Sakai M., Tamaki S., Hara H., Taki
Sawasaki Y., Hanada K.;
"Characterization of single chain urokinase-type plasminogen
activator with a novel amino-acid substitution in the kringle
structure.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRUCTURE BY NMR OF 67-155
MEDLINE=94149701; PubMed=8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Li X., Smith R.A.G., Dobson C.M., "Sequential IH NMR assignments ar domain from urokinase.", Biochemistry 31:9562-9571(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thromb. Haemost.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                urokinase-type plasminogen activator.";
Structure 3:681-691(1995).
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MEDLINE-93003110; PubMed-1
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                                                                                                                                                 TRYPSIN FAMILY.
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78:973-973(1997)
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∵~le domain
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om urokinase-type
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RESULT 3
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DT 01-FEB-1994 (Rel
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Best Local S
Matches
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PFAM: PF00089; trypsin; 1.

PRINTS: PR00722; CHYMOTRYPSIN.

SMART; SM00130; KR; 1.

SMART; SM00130; KR; 1.

SMART; SM00020; Tryp_SPC; 1.

PROSITE: PS010022; EGF_1; 1.

PROSITE: PS01016; EGF_2; PALSE_NEG.

PROSITE: PS01010; KRINGLE_1; 1.

PROSITE: PS00070; KRINGLE_2; 1.

PROSITE: PS0013; TRYPSIN_DOW; 1.

PROSITE: PS0013; TRYPSIN_HIS; 1.
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SIGNAL 1
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9 RHRGGS 20
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M13476; AAA61233.1; -...

D00244; BAA00175.1; -...

K03226; AAC97138.1; -...

K03226; AAC97138.1; -...

K03286; AAA61222.1; -...

A22571; CAN01599.1; -...

A28397; CAN01390.1; -...
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A32974; A32974.
1KDU; 31-OCT-93.
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1URK; 08-MAY-95
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6; Conser
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IPR000561; EGF-like.
IPR000001; Kringle.
IPR001254; Trypsin.
(Rel. 28, Created)
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                 STANDARD;
                                                                                                                                                                                                                                                                                                                                              3D-structure
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EGF-LIKE
KRINGLE.
CONNECTOR PLASMINOGEN AU BEGF-LIKE
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CLEAVAGE (DURING 2XM
SERINE PROTEASE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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Pred.
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UROKINASE-TYPE PLASMINOGEN
LONG A CHAIN.
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                                                                                                                                                                                    INTERCHAIN
                                                                                                   Mismatches
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                                                                                                           34; DB No. 5.8;
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  PRINTS; PRO0722; CHYMOTRYPSIN.
SMART; SM00130; KR; 1.
SMART; SM00020; TYPP_SPC; 1.
PROSITE; PS01186; ECF_2; FALSE_NEG.
PROSITE; PS01186; ECF_2; FALSE_NEG.
PROSITE; PS00012; KRINGLE_1; 1.
PROSITE; PS00013; KRINGLE_2; 1.
PROSITE; PS00244; TRYPSIN_DOM; 1.
PROSITE; PS00145; TRYPSIN_DISS; 1.
PROSITE; PS00145; TRYPSIN_HIS; 1.
PROSITE; PS00115; TRYPSIN_HIS; 1.
PROSITE; PS00115; TRYPSIN_HIS; 1.
 SIGNAL
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InterPro; IPR000561; EGF-1ke.
InterPro; IPR000001; Kringle.
InterPro; IPR001254; Trypsin.
Pfam; PF00051; Kringle; 1.
Pfam; PF00089; trypsin; 1.
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EMBL; X85801; CAA59796.1;
PIR; JN0560; JN0560.
HSSP; P00749; ILMW.
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RAYN P., Berglund L., Petersen T.E.;
RAYN P., Berglund L., Petersen T.E.;
"Cloning and characterization of the bovine plasmi and tpa.";
Int. Dairy J. 5:605-617(1995).
Int. Dairy J. 5:605-617(1995).
Int. CATALYTIC ACTIVITY: SPECIFIC CLEAVAGE OF ARG-|
PLASMINOGEN TO FORM PLASMIN.
INDUCTION: BY RETINOIC ACID.
I- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
I- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; AL:
TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                     "Bovine urokinase-type plasminogen activator and its receptor: cloning and induction by retinoic acid."; Gene 125:177-183(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1994 (Rel. 28, Last
01-NOV-1997 (Rel. 35, Last
UROKINASE-TYPE PLASMINOGEN
(U-PLASMINOGEN ACTIVATOR).
                                                                                                                                                                                                                                                                                                           SEQUENCE OF 12-433 FROM N.A. TISSUE-Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-AORTIC endothellum;
MEDLINE-93216119; PubMed-8385052;
Kraetzschmar J., Haendler B., Kojima
Schleuning W.-D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EQUENCE FROM N.A.
ISSUE-Aortic endothelium;
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ACTIVATOR PRECURSOR (EC 3.4.21.73) (UPA)
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                                                                                                                                                                                                                                                         plasminogen
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                                         ALSO KNOWN
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UROKINASE-TYPE PLASMINOGEN A CHAIN A (BY SIMILARITY).
CHAIN B (BY SIMILARITY).
EGF-LIKE.
KRINGLE.
CONNECTING PEPTIDE.
SERINE PROTEASE.

serine protease; Glycoprotein; Zymogen.

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CTISSUE-Thoracic aorta;

AN INFERENCE FROM N.A.

CTISSUE-Thoracic aorta;

AN INFERENCE FROM N.A.

COMEDINE-90287734; PubMed-2113276;

AN Y.P.T., Wang T.W., Clowes A.W.;

PUCLECTION AND T.W., Clowes A.W.;

PLASHINGSEN AND ENGLISH CLEAVAGE OF ARG-|-VAL BOND IN CLEAVAGE OF ARG-|-VAL BOND IN CLEAVAGE OF ARG-|-VAL BOND IN CLEAVAGE OF THO CHAINS.

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Best Local Similarity 100.0%;
Matches 6; Conservative 0
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Papio.
MCBI_TaxID=9556;
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p16227;
01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
UROKINASE-TYPE PLASMINGEN ACTIVATOR PRECURSOR (EC.
(U-PLASMINGEN ACTIVATOR).
                                                       EMBL; x51935; CAA36200.1;
PIR; S14687; UKBAY.
HSSP; P00749; 1LMW.
MEROPS; S01.231; -.
                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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IPR000561;
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Pred. No. 5.9;
D; Mismatches
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RESULT
UROK_PIG
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Best Local S
Matches 6
SEQUENCE FROM N.A.

TISSUE-Kidney;
MEDLINE-85087954; PubMed-6096832;
MEDLING-85087954; PubMed-6096832;
Nagamine Y., Pearson D., Altus M.S., Rei
CDNA and gene nucleotide sequence of po
Nucleic Acids Res. 12:9525-9541(1984).

[2]
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InterPro; IPRO00254; Trypsin.
Pfam; PF00051; Kringle; 1.
Pfam; PF00059; trypsin; 1.
Pfam; PF00089; trypsin; 1.
PRO0172; CHYMOTRYPSIN.
SMART; SM00181; EGF; 1.
SMART; SM00180; KR; 1.
SMART; SM00130; KR; 1.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS00022; EGF_1; FALSE_NEG.
PROSITE; PS00186; EGF_2; FALSE_NEG.
PROSITE; PS00186; EGF_2; FALSE_NEG.
PROSITE; PS0018; KRINGLE_2; 1.
PROSITE; PS00174; TRYPSIN_LSS; 1.
PROSITE; PS0018; TRYPSIN_LSS; 1.
PROSITE; PS0018; TRYPSIN_LSS; 1.
PROSITE; PS0018; TRYPSIN_LSS; 1.
                                                                                                                                                                                                                                                                                                                                                                                               20-MAR-1987 (Rel. 04, Creates
13-AUG-1987 (Rel. 05, Last sa
20-AUG-2001 (Rel. 40, Last as
UROKINASE-TYPE PLASMINOGEN ACTIVATOR).
                                                                                                                                                                                                                         Sus scrofa (Pig).
Eukaryota; Metazoa; C
Mammalia; Eutheria; C
NCBI_TaxID-9823;
[1]
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P04185;
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SHORT A CHAIN (A1) (BY SIMILARITY).

CHAIN B (BY SIMILARITY).

EGF-LIKE.

KRINGLE.

CONNECTING PEPTIDE.

SERINE PROTEASE.

BY SIMILARITY.

BY SIMILA
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annotation update)
ACTIVATOR PRECURSOR
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Pred. No. 5.9
0; Mismatches
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porcine p
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Sus.
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Query Match
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SMART; SM00130; KR; 1.
SMART; SM00020; TYP_SPS; 1.
SMART; SM00020; EGF_1; 1.
PROSITE; PS01186; EGF_2; FALSE_NEG.
PROSITE; PS01186; EGF_2; FALSE_NEG.
PROSITE; PS01012; KRINGLE_2; 1.
PROSITE; PS02070; KRINGLE_2; 1.
PROSITE; PS01013; TRYPSIN_DOM; 1.
PROSITE; PS01134; TRYPSIN_HS; 1.
PROSITE; PS01135; TRYPSIN_HS; 1.
                                                                                                                                                                                                        COMPLICT
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CON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nagamine Y.;
Submitted (DEC-1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEROPS; S01
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Nagamine Y.
1 RHRGGS 6
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                                                   Similarity 100.
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                activation; Hydrolase; Serine protease; Glycoprotein;
F-like domain; Zymogen; Signal.
1 20
21 442 UROKINASE-TYPE PLASMINOGEN ACTIVATOR
21 18 CHAIN A (BY SIMILARITY).
190 442 CHAIN B (BY SIMILARITY).
29 65 EGF-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UKPG.
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                                                                                                                                                                                                    14; Chymotrypsin.
51; EGF-like.
01; Kringle.
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BY SIMILARITY.

CHARGE RELAY SYSTEM.

CHARGE RELAY SYSTEM.
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BY SIMILARITY.
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Pred. No. 6;
0; Mismatches
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SERINE PROTEASE.
N-LINKED (GLCNAC...
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                                                                                                                     1; Length 442;
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Query Match Best Local S Matches 5

Similarity 5; Conserv

Conservative

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Score Pred.

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Length 86 Indels

Mismatches 31; DB

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MOD_RES
CONFLICT
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                                             Neurotoxin;
SIGNAL
CHAIN
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
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"Scorpion toxins from Centruroides noxius and Tityus serrulatus."

"Primary structures and sequence comparison by metric analysis.";

Biochem. J. 229:739-750(1985).

-I- FUNCTION: BINDS TO SODIUM CHANNELS AND INHIBITS THE INACTIVATION

OF THE ACTIVATED CHANNELS, THEREBY BLOCKING NEURONAL TRANSMISSION

-I- SUBCELLULAR LOCATION: SECRETED:
-I- SIMILARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.

BETA-TOXIN SUBFAMILY.
                                                                                                                                                                                                           InterPro; IPR003614; Knot1.
InterPro; IPR002061; Scorpion_toxin.
InterPro; IPR001209; Toxin.
Pfam; PF00537; toxin_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND AMIDATION.

MEDLINE-96119048; PubMed-8585086;

Vazquez A., Tapia J.V., Eliason W.K., Martin B.M., Lebreton F.,

Delepierre M., Possani L.D., Becerril B.;

"Cloning and characterization of the cDNas encoding Na+
channel-specific toxins 1 and 2 of the scorpion Centruroides noxius
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CENNO STANDARD; PRT; STANDARD; PRT; STANDARD; PRT; STANDARD; O1-APR-1990 (Rel. 14, Created) STANDARD; PRT; O1-APR-1998 (Rel. 37, Last sequence up 20-AUG-2001 (Rel. 40, Last annotation TOXIN 1 PRECURSOR (TOXIN 11.14) (CN1).
                                                                                                                                                   ProDom; PD000908;
SMART; SM00505; Kr
                                                                                                                                                                                                                                                                      EMBL; S81093; AAB36085.2; -. PIR; S32789; S32789. HSSP; P01492; IVNA.
                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Centruroides noxius (Mexican scorpion).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthoidea; Buthidae; Centruroides.
                                                                                                                                                                                  PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 20-84.
MEDLINE-86025386; PubMed-4052021;
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                                                                                                                                                                                PR00284; TOXIN.
PR00285; SCORPNTOXIN
                                                                                                                                      Sodium
 &
                                                                                                                                                   8; Scorpion_toxin; 1.
Knot1; 1.
                                                                                                                                      channel inhibitor; Amidation; Signal
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
ANIDATION (G-85 PROVIDE AMIDE GROUP).
P -> T (IN REF. 2).
ABBC1EA742F17222 CRC64;
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on update)
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Best Local
                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCX7_CENNO
P45665;
01-NOV-1995
01-NOV-1995
20-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CENNO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Cloning and characterization of cDNAs that code for Na(+)-channel-blocking toxins of the scorpion Centruroides noxius Hoffmann."; Gene 128:165-171(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
TOXIN ONGTIV PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L05062; AAA28287.1; -. HSSP; P01494; 2SN3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Centruroides noxius (Mexican scorpion)
Eukaryota; Metazoa; Arthropoda; Chelic
Buthoidea; Buthidae; Centruroides.
                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neurotoxin;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00537;
PRINTS; PR0028
                                                                                                                                                                                                                                                                                                                                                         MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003614; Knot1.
InterPro; IPR002061; Scorpion_toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Possani L.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-93292983; PubMed-8390386;
Becerril B., Vazquez A., Garcia C., Corona M., Bolivar F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-6878;
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                                                                                                                                           1 RHRGGS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PUNCTION: BINDS TO SODIUM CHANNELS AND INHIBITS THE INACTIVA OF THE ACTIVATED CHANNELS, THEREBY BLOCKING NEURONAL TRANSMI SUBCELLULAR LOCATION: SECRETED.
SIMILARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BETA-TOXIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RHRGGS
                                                                                                KHRGGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KHRGGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PR00284; TOXIN.
PR00285; SCORPNTOXIN.
PD000908; Scorpion_to
                                                                                                                                                                                        Similarity
5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        non-profit institutions as long as its content
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                                                                                                                                                                                           Conservative
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30
34
43
47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8; Scorpion_toxin; Knot1; 1.
                                                                                                                                                                                                                                                                                                                                                 n channel inhibitor; Amidation; Signal.

19 BY SIMILARITY.

84 TOXIN CHORITY.

85 BY SIMILARITY.

59 BY SIMILARITY.

66 BY SIMILARITY.

66 BY SIMILARITY.

68 AMIDATION (G-85 PROVIDE AMIDE GROUP)
                                                                                                                                                                                                                                                                                                              9560
                                                                                                                                                                                                              91.2%;
83.3%;
                                                                                                                                                                                                                                                                                                              ₹.
                                                                                                                                                                                     Score 31; DB
Pred. No. 4.8;
1; Mismatches
                                                                                                                                                                                           <u>:</u>
                                                                                                                                                                                                                                                                                                           (POTENTIAL).
4D6BA41F905EBBD0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chelicerata; Arachnida; Scorpiones;
                                                                                                                                                                                                                4.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AND INHIBITS THE INACTIVATION BLOCKING NEURONAL TRANSMISSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ₹
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Best Local S
Matches 5
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Bacteria; Proteo
Haemophilus.
NCBI_TaxID=727;
[1]
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01-NOV-1995
20-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;
"Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";
                                                                                                                                                                                                        TRANSMEM
TRANSMEM
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TRANSMEM
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00610; NA_NEUROTRAN_SYMP_1; 1.

PROSITE; PS00754; NA_NEUROTRAN_SYMP_2; FALSE_NEG.

PROSITE; PS50267; NA_NEUROTRAN_SYMP_3; 1.

Hypothetical protein; Transport; Transmembrane: S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
Pfam; PFOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities regulares a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
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P44849;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-RD / KW20 / ATCC 51907;
MEDLINE-95350630; PubMed-7542800;
Fleischmann R.D. Adams M.D. Whi
Kerlavage A.R., Bult C.J., Tomb J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U32757; AAC22395.1; TIGR; HI0736; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHET ICAL
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                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RANSMEM
74 RHRGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FAMILY (SNF).
                          RHRGGS 6
                                                                                        Similarity
5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR000175; Na_neurotran_symport
0209; SNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       us influenzae.
Proteobacteria;
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5 (Rel. 32, Last sequence of the control of t
  79
                                                                                           Conservative
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                                                                                                             91.2%;
                                                                                                                                                                                                             55177
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Last annotation update)
EPENDENT TRANSPORTER HI0736.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D., White O., Clayton R.A., Kirkness E.F., Tomb J.-F., Dougherty B.A., Merrick J.M., tzhugh W., Fields C.A., Gocayne J.D.,
                                                                                        ; Score 31; DB; Pred. NO. 30; 1; Mismatches
                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                             5CC50526DE854BB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane; Symport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  508
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                                                                                                                                       ۲,
                                                                                                                                       Length 508
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in no way
commercial
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STRUCTURE REPORTED CONTROL CON
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Best Local
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SMART; SM00382: AAA; 1.
PROSITE; PS01008; DNAA; 1.
DNA replication; DNA-binding; A
NP_BIND 344 351
SEQUENCE 643 AA; 71317 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNAA_STRRE
Q9ZH76;
20-AUG-2001
20-AUG-2001
20-AUG-2001
                                                                                                                                                                                                                     P52623;
01-OCT-1996 (Rel. 34
01-OCT-1996 (Rel. 34
15-JUL-1999 (Rel. 38
URIDINE KINASE (EC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF071023; AAD08806.1; -.
Interpro; IPR003593; AAA.
Interpro; IPR001957; Bac_DnaA.
Pfam; PF00308; bac_dnaA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces reticuli.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CHROMOSOMAL REPLICATION INITIATOR PROTEIN DNAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JAN-1999)
-!- FUNCTION: PLAYS A
                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zakrzewska-Czerwinska
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Majka J., Jakimowicz D., Messer W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-TU45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID-1926;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNAA
SEQUENCE FROM TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                            URK1_MOUSE
                                                                                                                                                                                                UMPK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 RHRGGA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interactions of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RHRGGS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mitted (JAN-1999) to the EMBL/GenBank/DDBJ databases. PUNCTION: PLAYS AN IMPORTANT ROLE IN THE INITIATION AND REGULATION OF CHROMOSOMAL REPLICATION. BINDS TO THE ORIGIN OF REPLICATION; IT BINDS SPECIFICALLY DOUBLE-STRANDED DNA AT A 9 BE CONSENSUS (DNAA BOX): 5'TTATC(C/A)A(C/A)A-3'. DNAA BINDS TO ATP AND TO ACIDIC PHOSPHOLIPIDS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE DNAA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 83. 5; Conservative
                           N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                     34, Created)
34, Last sequence update)
38, Last annotation update)
C 2.7.1.48) (URIDINE MONOPHOSPHOKINASE) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91.2%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptomyces lividans initiator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 31; DB
; Pred. No. 38;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP-binding
                                                                                                       Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                               PRT;
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DB9E173DF24758B5 CRC64;
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                                                                                                             Euteleostomi;
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01-MAY-1991
30-MAY-2000
CHLOROPLAST
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P21434;
                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                       EMBL;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
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Ropp P.A., Traut T.W.;
"Cloning and expression of a cDNA encoding uridine kinase
                                                                                                                                                                                                                                                                                                                                                                               Nucleic Acids Res. 12:6547-6558(1984).
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CATALYTIC ACTIVITY: ATP + URIDINE - ADP + UMP.
PATHMAY: PYTAYIDINE SALVAGE PATHWAY.
SIMILARITY: BELONGS TO THE URIDINE KINASE FAMILY.
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                                                                        ; X00798; CAB523
S07356; R5NT2D.
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milarity 100.0%;
Conservative
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(Rel. 18, Last sequence update)
(Rel. 39, Last annotation update)
50S RIBOSOMAL PROTEIN L2.
                                                                                                          CAB52367.1; -.
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PIR;

Mendel; 5309; NICde;rpl2;1.
InterPro; IPR002171; Ribosomal\_L2
Pfam; PF00181; Ribosomal\_L2; 1.

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                                                       RK2_SPIOL STANDARD: PRT; 271 AA.
P065509; Q9H1V0; Q9M3I1;
01-JAN-1988 (Rel. 06, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CHLOROPLAST 50S RIBOSOMAL PROTEIN L2 (RIBOSOMAL PROTEIN CS-L4).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-19 FROM A. A. MEDLINE-88203193; PubMed-3362671; Thomas F., Massenet O., Dorne A.M., Briat J.F., Expression of the rp123, rp12 and rps19 genes in the second 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-CV. GEANT D'HIVER, AND CV. MONATOL;
MEDLINE-21187424; PubMed-11292076;
MEDLINE-21187424; PubMed-11292076;
Schmitz-Linneweber C., Maier R.M., Alcaraz J.-P., Cottet A.,
Herrmann R.G., Mache R.;
"The plastid chromosome of spinach (Spinacia oleracea): complete
nucleotide sequence and gene organization.";
Plant Mol. Biol. 45:307-315(2001).
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"Complete identification of ribosomal proteins
an organelle (chloroplast) ribosome.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ d
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N.BI_TaxID=3562;
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5; Conser
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l protein; Chloroplast.
266 AA; 28901 MW; 8F4
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milarity 100.08;
Conservative 0,
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Pred. No.
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RESULT 13
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ID RKZ_HORVU
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DT 01-FEB
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Matches
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P41096;
01-FEB-1995
01-FEB-1995
01-FEB-1996
CHLOROPLAST
    Pfam; PF00181; Ribosomal_L2; 1.
PROSTIE; PS0046; RIBOSOMAL_L2; 1.
Ribosomal protein; Chloroplast.
SEQUENCE 273 AA; 30045 MA; 4C2
                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN-CY. BAISA;
MEDLINE-95086380; PubMed-7994178;
Hess W.R., Hoch B., Zeltz P., Hue
Boerner T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euxaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldea Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INIT_MET
MOD_RES
SEQUENCE
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EMBL; AJ400848; CAB88803.1; -.
EMBL; X07462; CAA30345.1; -.
PIR; S07918; R5SP2.
PIR; S07918; R5SP2.
Mendel; 4699; SPIO1; P12; 1.
                                                                                                                                                                                        EMBL; X78185;
Mendel; 4044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Inefficient rp12 splicing in barley mutants with ribosome-deficient plastids."; plant cell 6:1455-1465(1994).
-i- SIMILARITY: BELONGS TO THE L2P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hordeum vulgare (Barley).
Chloroplast.
Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002171; Ribosomal_L2.
Pfam; PF00181; Ribosomal_L2; 1.
PROSITE; PS00467; RIBOSOMAL_L2; 1.
                                                                                                                                                   Mendel; 4044; HORvu;rpl2;1.
InterPro; IPR002171; Ribosomal_L2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID-4513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ribosomal protein; Chloroplast; Methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RHRGG
||-|||
47 RHRGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 31, Created)
(Rel. 31, Last sequence update)
(Rel. 33, Last annotation updat
50S RIBOSOMAL PROTEIN L2.
                                                                                                                                                                                                                             CAA55028.1; ALT_SEQ.
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100.0%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              METHYLATION (MONO-).
; B8E06EC44FD93B63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Huebschmann T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
            4C204966ACB7DBE9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Koessel H.
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Query Match Best Local Similarity

88.2%;

Score

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26;

1;

Length 273;

RESULT 14

RK2\_MAIZE P17788;

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50

RHRGG

Matches

5

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EMBL; X53066; CAA37241.1; -
EMBL; X86563; CAA6039.1; A
EMBL; X86563; CAA60371.1; -
EMBL; X62070; CAA43983.1; A
PIR; S10500; R52M2.
PIR; S17874; S17874.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
NCBI_TaxID-4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE-95395841; PubMed-7666415;

MALET R.M., Neckermann K., Igloi G.L., Koessel H.;

MICOMPLETE SEQUENCE: General G. K., Koessel H.;

MEDLINE-95395841; Florida G. K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-90332419; PubMed-2377464; Kavousi M., Giese K., Larrinua I.M., Subramanian A.R.; Ravousi M., Giese K., Larrinua I.M., Subramanian A.R.; Nucleotide sequence and map positions of the duplicated matre (Zea mays) chloroplast ribosomal protein L2.*; nucleic Acids Res. 18:4244-4244(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-91367263; PubMed-1653905; Hoch B., Maier R.M., Appel K., Igloi G.L., "Editing of a chloroplast mRNA by creation Nature 353:178-180(1991).
                                                                                                                       Pfam; PF00181; Ribosomal_L2; 1.
PROSITE; PS00461; RIBOSOWAL_L2; 1.
RIBOSOMAL Protein; Chloroplast; RNA editing.
RIBOSOMAL PROTEIN; BA65197231EA3CAO CRC64;
SEQUENCE 273 AA; 30065 MW; BA65197231EA3CAO CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-CV. FR9CMSSR37;
                                                                                                                                                                                            Mendel; 11440; ZEAma;rpl2;1.
InterPro; IPRO02171; Ribosomal_L2;
Pfam; PF00181; Ribosomal_L2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EDITING OF INITIATOR CODON
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88.2%; Silarity 100.0%; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                               ALT_SEQ
                                                                                                                                                                                                                                                                                                                                                                                           ALT_SEQ
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                        Score 30;
Pred. No.
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                           DB 1;
26;
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                                            Length 273;
  Indels
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  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                          EMBL; X15901; CAA33924.1;
EMBL; X15901; CAA33928.1; A
EMBL; M2826; CAB25244.1; A
EMBL; L40578; AAD15254.1; A
PIR; JQ0270; R5R22.
Mendel; 5002; OKYBa; Fp12;1.
InterPro; IPR002171; Riboso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RK2_ORYSA STANDARD; PRT; 273 AA P17351; P92327; 01-AUG-1990 (Rel. 15, Created) 01-AUG-1990 (Rel. 15, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) CHLOROPLAST 505 RIBOSOMAL PROTEIN L2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between the Swiss Institute of Bioinformat
the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
entitles requires a license agreement (See
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hiratsuka J., Shimada H., Whittier R., Ishibashi T., Sakamoto M., Mori M., Kondo C., Honji Y., Sun C.-R., Meng B.-Y., Li Y.-Q., Kanno A., Nishizawa Y., Hirai A., Shinozaki K., Sugiura M.; "The complete sequence of the rice (Oryza sativa) chloroplast genome: intermolecular recombination between distinct tRNA genes accounts for a major plastid DNA inversion during the evolution of the cereals."; amajor plastid DNA inversion during the evolution of the cereals."; mol. Gen. Genet. 217:185-194(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-CV. NIPPONBARE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa (Rice).
Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the rice chloroplast genome.";
Gene 70:1-12(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE-89196901; PubMed-3240862;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPLETE GENOME.
MEDLINE-89364698; PubMed-2770692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sugiura M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RPL2-A AND RPL2-B
                                                                                                   SEQUENCE
                                                                                                                                             CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted
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                                                                                                                                                                                                                                              ; IPR002171; Ribosomal_L2.
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PS00467; RIBOSOMAL_L2; 1.
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  Score 30;
Pred. No.
                                                                                                Q -> E:(IN REF. 3).
Q -> K (IN REF. 3).
HGGGEGKAPIGKKPTT -> GAVKGKPPLVEKNPQP
(IN REF. 3).
AA4153C62AA8729B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (See http://www.isb-sib.ch/announce/
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Query Match Best Local S Matches 5

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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RHRGG 5
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Db 50 RHRGG 54

Search completed: March 18, 2002, 09:52:24

Job time: 293 sec
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Q9SI97 Q9I6I1 Q9XMU4 Q9ZIL2 Q9ZIL2 Q9F2Q1 Q9F2Q1 069724 085283

Q9f2q1 streptomyce O69724 mycobacteri O85283 sphingomona

Q9xmu4 Q9z112 Q9f2q1

myxococcus tetrahymena

Q9si97 arabidopsis Q916il pseudomonan

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Q9W228 Q69558 Q9V6Y6 0 Q41927 2 Q9Q0D0 2 Q9Q0C9 1 Q63730

065929 daucús caro
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09v6y6 drosophila
041927 arabidopsis
09400 herpes simp
09300 herpes simp
063730 rattus norv
09p663 neurospora
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09v6r2 drosophila

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09xt70 oryctolagus
015844 homo sapien
016618 homo sapien
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09up84 homo sapien
017240 bombyx mori
045599 caenorhabdi
09puM4 gallus gall
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BIOChem. Biophys. Res. Commun. 252:757-763(1998).

C --- SIMILARITY: TO SERINE PROTEASES, TRYPSIN FAMILY.

C --- SIMILARITY: TO CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1).

R EMBL; AF069711; AAC95003.1; ---

R InterPro; IPR001314; Chymotrypsin.

R InterPro; IPR001324; Trypsin.

R InterPro; IPR001254; Trypsin.

R PF6am; PF00089; Trypsin.

R PRINTS; PR00722; CHYMOTRYPSIN.

R PROSITE; PS00134; TRYPSIN.

R SAART; SM0020; Tryp. SPC; 1.

R PROSITE; PS00134; TRYPSIN.BIS; UNKNOWN_1.

R PMOSITE; PS00134; TRYPSIN.BIS; UNKNOWN_1.
                                               Query Match 100.0%; Best Local Similarity 100.0%; Matches 6; Conservative 0;
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SEQUENCE
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097587;
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STRAIN-NEW ZEALAND WHITE;
MEDLINE=99057575; PubMed=9837780;
Reno C., Boykiw R., Martinez M.L., Hart D.A.;
"Temporal alterations in mRNA levels for proteinases and inhibitors and their potential regulators in the healing medial collateral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID-9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-1999 (TEXMBLrel. 10, Created)
01-MAY-1999 (TEXMBLrel. 10, Last sequence update)
01-UN-2001 (TEXMBLrel. 17, Last annotation update)
UROKINASE (FRAGMENT).
   1 RHRGGS 6
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128 AA;
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14328 MW;
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Score 34; DB Pred. No. 10; ); Mismatches

6; 0;

Length 128; Indels

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InterPro: IPR000001; Kringle.
InterPro: IPR001254; Trypsin.
Pfam; PP00051; Kringle; 1.
Pfam; PP00089; trypsin; 1.
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Q9XT70;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
UROKINASE-TYPE PLASHINGGEN ACTIVATOR (FRAGMENT).
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PROSITE; PS00021; KRINGLE_1; 1.
PROSITE; PS50070; KRINGLE_2; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalla; Eutheria; Lagomorpha; Leporidae; Oryotolagus.
                                                                         Nagai M., Hiramatsu R., Kaneda T., Hayasuke Nishida M., Suyama T.;
*Molecular cloning of cDNA coding for human Gene 36:183-188(1985).
                                                                                                                                                                                                                                                    Homo sapiens (Human),
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
MCBI_TaxID=9606;
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NON_TER 214
SEQUENCE 214 AA;
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SMART; SM00130; KR; 1.
SMART; SM00020; Tryp_S
SEQUENCE FROM N.A. MEDLINE-96186279; PubMed-8652631;
                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-86056954; PubMed-2415429;
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ilarity 100.0%;
Conservative (
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17;
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Best Local S
Matches 6
                                   MEDLINE-8520359; PubMed-3888571;
MEDLINE-8520359; PubMed-3888571;
Jacobs P., Cravador A., Loriau R., Brockl;
Van Elsen A., Herzog A., Bollen A.;
"Molecular cloning, sequencing, and exprehuman preprourokinase cDNA.";
DNA 4:139-146(1985).
-I- SIMILARITY: TO SERINE PROTEASES, TRYP.
-I- SIMILARITY: TO CHYMOTRYPSIN SERINE PREMBL; X02760; CAAA65351; -.
HSSP. P00749; IURK.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR0001314; Chymotrypsin.
InterPro; IPR0001254; Trypsin.
Pfam; PF00081; kringle.
InterPro; IPR0001254; Trypsin.
Pfam; PF00081; kringle: 1.
Pfam; PF00081; kringle: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; PUV/49; LVAN.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR000561; EGF-11ke.
InterPro; IPR000001; Kringle.
InterPro; IPR002254; Trypsin.
Pfam; PF00051; kringle; 1.
Pfam; PF00051; kringle; 1.
Pfam; PF00052; CHYMOTRYPSIN.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00018; KRINGLE.
SMART; SM00181; EGF; 1.
SMART; SM001002; EGF_1; 1.
PROSITE; PS00022; EGF_1; 1.
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NON_TER
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q16618
Q16618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              with a novel amino-acid substitution in biochim. Biophys. Acta 1293:83-89(1996) -- SIMILARITY: TO CHYMOTRYPSIN SERINE -- SIMILARITY: TO CHYMOTRYPSIN SERINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TREMBLIFEL 01, Created)
01-NOV-1996 (TREMBLIFEL 01, Last seq
01-JUN-2001 (TREMBLIFEL 17, Last and
UROKINASE PRECURSOR (EC 3.4.99.26).
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HSSP; P00749;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00022;
PROSITE; PS00021;
PROSITE; PS50070;
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Sawasaki Y., Hanada K.;
"Characterization of single chain
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE-85203359;
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6; Conserv
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411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BAA01919.1; -.
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                    CHYMOTRYPSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46383 MW;
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17, Last annotation
3.4.99.26).
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Pred. No. 33;
Nismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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F99AD080FD43FC96 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                       Brockly F.,
                                                                                                                                                                                                                                                                                                                        expression
                                                                                                                                                                                                                                 TRYPSIN FAMILY.
NE PROTEASE FAMILY (S1).
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Best Local S
Matches 6
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PROSITE; PS00022; EGE 1; 1.

PROSITE; PS00021; KRINGLE_1; 1.

PROSITE; PS50070; KRINGLE_2; 1.

PROSITE; PS00134; TRYPSIN_HIS; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                     O90G84 PRELIMINARY; PRT; 597 AA.

G9UG84:
01-MAY-2000 (TIEMBLITEL 13, Created)
01-MAY-2000 (TIEMBLITEL 13, Last sequence update)
01-JUN-2001 (TIEMBLITEL 17, Last annotation update)
HYPOTHETICAL 66.7 KDA PROTEIN (FRAGMENT).

DKFZP564A1523........
                                                                                                                                                                                                                                                                                                                          EMBL; AF1
NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                           Schiff M., Siderovski D., Jordan J.D., Brothers G., Snow B., Dho S., Wolting C., McGlade J., De Vries L., Ortiz D., Diverse-Pieriuissi M.; "GABA B receptor-induced N-type calcium channel modulation is mediate by interactions of the PTB domain of RGS12 with the tyrosine-phosphorylated channel."; Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TIEMBLrel. 13, Created)
01-MAY-2000 (TIEMBLrel. 13, Last sequence update)
01-MAY-2000 (TIEMBLrel. 13, Last sequence update)
01-MAY-2000 (TIEMBLrel. 13, Last annotation update)
N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (FRAGMENT).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase; Serine protease; Signal.
SIGNAL 1 20 POTENTIAL.
CHAIN 21 431 UROKINASE.
SEQUENCE 431 AA; 48664 MW; 16082504B57AC18B
                                                                                                                                                                                                              1 RHRGGS 6
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248 RHRGGS 25
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SMART; SM00020;
                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID-9031;
  SEQUENCE FROM N.A
                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EQUENCE FROM N.A.
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Similarity 100.
6; Conservative
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nilarity 100.0
Conservative
                                                                                                                                                                                                                                                                                                                           444 AA;
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50547 MW;
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Pred. No.
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Pred.
                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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No.
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                                                                                                                                                                                                                                                                                      Length 444;
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Best Local S
Matches
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Best Local S
Matches 6
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submitted (MAY-1999) to the EMBL/GenBanl
EMBL; ALO49954; CAB4323-1; -
HSSP; P10760; 1B3R.
Interpro; IPR001043; Ado_hcyase.
Interpro; IPR001220; Lectin_legB.
Interpro; IPR001220; Lectin_legB.
Pfam; PF00670; AdoHcyase; 1.
PR0SITE; PS00738; ADOHCYASE_1; 1.
PR0SITE; PS00739; ADOHCYASE_2; UNKNOWN_
PROSITE; PS00307; LECTIN_LEGUME_BETA; UI
                                                                                                                                                                                                                                                                                             045599 PRELIMINARY:
045599; 01-JUN-1998 (TrEMBLrel. 0
01-JUN-1998 (TrEMBLrel. 0
01-JUN-2001 (TrEMBLrel. 1
H02112.1 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-EUROPEAN 200X300; TISSUE-MEDIAN SILK GLAND;
GREEL A.A., Deleage G.G., Prudhomme J.J.;
Garel A.A. (MAR-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; Z48802; CAA88741.1;
EMBL; Z48802; CAA88741.1;
SEQUENCE 1217 AA; 123410 MM; 4C5789F87F6866D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q17240
Q17240;
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01-NOV-1996 (TrEMBLrel
01-NOV-1996 (TrEMBLrel
SERICINIB
                                                                                                                        Eukaryota; Metazoa; Nematu
Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bombyx mori (Silk moth).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Bombycoidea, Bombycidae; Bombyx.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
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Wambutt R., F
McLay K.;
Submitted (MAR-1997)
                                                                                                                                                                                                                                    Caenorhabditis elegans.
                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=7091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              731
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Similarity 100.0%;
6; Conservative (
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6; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                     Nematoda; Chromadorea; rinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66668 MW;
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01, Last sequence update)
01, Last annotation updat
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the EMBL/GenBank/DDBJ databases
3.1; -.
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06,
17,
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Last sequ
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Pred. No. 99;
); Mismatches
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Pred.
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E_BETA; UNKNOWN_1
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No.
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                                                                                                                                                                                                          Rhabditida; Rhabditoidea;
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Best Local S
Matches 6
                                                                                                         Matches
                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9PUM3 PRELIMINARY; PAL, 2010M3; Q9PUM3; Q1-MAY 2000 (TrEMBLrel. 13, Created) Q1-MAY 2000 (TrEMBLrel. 13, Last sequence update) Q1-JUN 2001 (TrEMBLrel. 17, Last annotation update) N-TYPE CALCIUM CHANNEL ALPHA-1B CDB4 VARIANT.
                                                                                                                                                                                                                                                                                                Lu Q., Dunlap K.;

Cloning and Functional Expression of Novel N-type Ca2+ Channel Variants "
J. Biol. Chem. 274:34566-34575(1999).

EMBL; AF173015; AAD51818.1; ".

InterPro; IPR000565; CatLon_chan_non_lig.

InterPro; IPR001682; Channel_pore_Ca_Na.

InterPro; IPR001695; Na_channel.

InterPro; IPR00177; Ca_channel.

InterPro; IPR002077; Ca_channel.

InterPro; IPR002071; Ca_channel.

InterPro; IPR002071; Ca_channel.

InterPro; IPR002071; Ca_channel.

InterPro; IPR002071; Ca_channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE-DORSAL ROOT GANGLION NEURONS;
MEDILINE-20044702; PubMed-10574919;
Lu Q., Dunlap K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Watson A., werman.
*2.2 Mb of contiguous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Z92789; CAB07215.1; -.
InterPro; IPRO02557; Chitin_binding
Pfam; PF01607; Chitin_bind_2; 9.
SMART; SM00494; ChtBD2; 12.
SEQUENCE 1332 AA; 145729 MW; 3D:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9031;
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SEQUENCE FROM N.A.
   947
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Local Similarity 100.
hes 6; Conservative
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                                                   RHRGGS 6
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RHRGGS
                                                                                                                                                                                                                                    PR00167; CACHANNEL.
PR00170; NACHANNEL.
E 2146 AA; 244649
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6; Conser
952
                                                                                                         100.0%;
ilarity 100.0%;
Conservative (
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                                                                                                      Score 34; DB
Pred. No. 1.7
); Mismatches
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Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                          281BBECAC494AE49 CRC64;
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                                                                                                      DB 13;
1.7e+02;
thes 0;
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                                                                                                                                                      Length 2146;
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Best Local S
Matches 6
                                     J. Biol. Chem. 0:0-0(1999).
EMBL; AF773017; AAD51820.1;
InterPro; IPR000636; Cation_chan_non_lig.
InterPro; IPR001682; Channel_pore_Ca_Na.
InterPro; IPR001695; Na_channel.
InterPro; IPR002077; Ca_channel.
InterPro; IPR00211; Cat_channel_TrpL.
Pfam; PF00520; ion_trans; 4.
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J. Biol. Chem. 0:0-0(1999).
EMBL; AF173019; AAD51822.1; -
InterPro; IPR001656; Cation_chan_non_lig.
InterPro; IPR001682; Channel_pore_Ca_Na.
InterPro; IPR001696; Na_channel.
InterPro; IPR002077; Ca_channel.
InterPro; IPR002111; Cat_channel_TrpL:
InterPro; IPR001111; Cat_chan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9PW44

Q9PW44

Q9PW44

Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
N-TYPE CALCIUM CHANNEL ALPHA-1B CDB8 VARIANT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TEQUENCE FROM N.A.
TISSUE-DORSAL ROOT GANGLION NEURONS;
Lu Q., Dunlap K.;
"Cloning and Functional Expression of
Variants.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
N-TYPE CALCIUM CHANNEL ALPHA-1B CDB6 VARIANT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata;
Archosauria; Aves; Neognathae.
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PRINTS; PR00170; NACHANNEL.
SEQUENCE 2157 AA; 245853 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9PW46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID-9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9031;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 100.0%;
Similarity 100.0%;
6; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neognathae;
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Pred. No. 1.8e+02;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Eute; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5E85C3AAF9493589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2157;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRC64;
                                                                                                                                                                                                                                                                                                                                                                            Ca2+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Euteleostomi;
idae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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RESULT 13
OSPUMA
ID OSPUMA
AC OSPUMA
DT 01-MAY
DT 01-MAY
DT 01-MAY
DT 01-GAILUS
CACHAI
OS GAILUS
OC EUKARY
OC EUKARY
OC GAILUS
OX NCBILIS
OX NCBILIS
OX NCBILIS
OX NCBILIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 6
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Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF173013; AAD51816.1;
InterPro; IPR000636; Cation_chan_non_lig.
InterPro; IPR001682; Channel_pore_Ca_Na.
InterPro; IPR001696; Na_channel.
InterPro; IPR002077; Ca_channel.
InterPro; IPR002011; Cat_channel_TrpL.
InterPro; IPR00211; Cat_channel_TrpL.
Pfam; PF00520; ion_trans; 4.
PRINTS; PR00157; CACHANNEL.
PRINTS; PR00157; CACHANNEL.
PRINTS; PR00167; CACHANNEL.
SEQUENCE 2182 AA; 248259 MW; 1C34F9DF59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00170; NACHANNEL. SEQUENCE 2171 AA; 247055 MW;
SEQUENCE FROM N.A. TISSUE-DORSAL ROOT GANGLION NEURONS
                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
N-TYPE CALCIUM CHANNEL ALPHA-1B CDB3 VARIANT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE-DORSAL ROOT GANGLION NEURONS;
MEDLINE-20044702; PubMed-10574919;
                                                                                                                                                                                     Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9PUM4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Biol. Chem. 274:34566-34575(1999).
EMBL; AF173013; AAD51816.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                          Q9PUM4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cloning and Functional Expression of Novel N-type Ca2+ Channel Variants."
                                                                                         NCBI_TaxID=9031;
                                                                                                                                                          Archosauria; Aves;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            983 RHRGGS 988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RHRGGS 6
||||||
972 RHRGGS 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RHRGGS 6 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q., Dunlap K.;
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6; Conservative (
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Similarity 100.0%;
6; Conservative (
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                                                                                                                                                          Neognathae;
                                                                                                                                                                                         Chordata;
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Pred. No. 1.8
0; Mismatches
                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; 
; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 34; DB 13;
Pred. No. 1.8e+02;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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. 1.8e+02;
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RESULT
Q9PW45
ID Q9
AC Q9
DT 01
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Best Local S
Matches 6
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Best Local Similarity 100.0%;
Matches 6; Conservative (
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InterPro; IPR001682; Channel_pore_Ca_Na.
InterPro; IPR001682; Channel.
InterPro; IPR001696; Na_channel.
InterPro; IPR002077; Cac_channel.
InterPro; IPR002111; Cat_channel_TrpL.
Pfam; PF00520; 1on_trans; 4.
PRINTS; PR00167; CACHANNEL.
PRINTS; PR00170; NACHANNEL.
SEQUENCE 2321 AA; 262972 MW; E6FB22:
                                                                                                                                                                                                                                                                                                                                                   J. Neurosci. 0:0-0(2000).

EMBL; AF17380; AAF2429.1; -...
InterPro; IPR001636; Cattion_chan_non_lig.
InterPro; IPR001692; Channel_pore_Ca_Na.
InterPro; IPR001696; Na_channel.
InterPro; IPR001996; Na_channel.
InterPro; IPR002077; Ca_channel.
InterPro; IPR002111; Cat_channel.TrpL.
Pfam; PF00520; ion_trans; 4.
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Q9TTA4;
Q9TTA4;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-WAY-2001 (TrEMBLrel. 17, Last annotation update)
N-TYPE CALCIUM CHANNEL ALPHAIB SUBUNIT.
Q9PW45;
Q9PW45;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; (
Mammalia; Eutheria; (
Bovidae; Bovinae; Bos NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Co-expression of cloned alphalB, beta2a, and alpha2/delta subunits produces non-inactivating calcium channels similar to those found in bovine chromaffin cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-20044702; PubMed-10574919;
Lu Q., Dunlap K.;
"Cloning and Functional Expression of
Variants.";
J. Biol. Chem. 274:34566-34575(1999).
EMBL; AF173014; AAD51817.1;
                                                                                                                                                                                                                                                                                                PRINTS; PRO0167; CACHANNEL.
PRINTS; PRO0170; NACHANNEL.
SEQUENCE 2331 AA; 260560 MW;
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                                                                                                                                962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         947 RHRGGS 952
                                                                                                                            1 RHRGGS 6
| | | | | |
962 RHRGGS 96
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                                                                                                                                                                                                      Similarity
6; Conserv
(TrEMBLrel. 13,
                                                                                                                                967
                                     PRELIMINARY;
                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                       100.0%;
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                                                                                                                                                                                                                           Score 34; DB 6;
Pred. No. 1.9e+0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 34; DB 13;
Pred. No. 1.9e+02;
; Mismatches 0;
                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                  6A7F35C35C45EED8 CRC64;
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                                       2332
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                                       ξ
                                                                                                                                                                                                                         .9e+02;
                                                                                                                                                                                                                                          Length 2331;
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DT 01-MAY-2000 (TREMBLICAL. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLICAL. 17, Last annotation update)
DE N-TYPE CALCIUM CHANNEL ALPHA-1B CDB7 VARIANT.

GN GACHALB.

OC GACHALB.

CE ENKARYCLE; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Gallus gallus (Chicken).

CC Gallus Seximine; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
CC Gallus.

OX NCBI_TAXID-9031;
RR 1010-TAXID-9031;
RR 1010-TAXID
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Beta plasminogen a Sequence of human

Plasminogen Activa

Human shear stress Human alpha-1-anti Thrombin inhibitor

Human

Plasminogen

PAI-1(E350-R). H
PAI-1(E351-R). H
Plasminogen activa

Human

n Plasminogen
1 (Arg 350) mu
1 (Arg 351) mu
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1 (Arg 351) mu
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1 (Arg 350) mu

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Title:
Perfect score:
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No.
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  of hits satisfying chosen parameters:
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2: /SIDSB/gcgdata,
3: /SIDSB/gcgdata,
4: /SIDSB/gcgdata,
5: /SIDSB/gcgdata,
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7: /SIDSB/gcgdata,
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Maximum Match 100%
Listing first 45 su
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| SIDSB/gcgdata/geneseq/geneseqp/AA1986 .DAT:*
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                                                                                                                                                   Description
Plasminogen activator inhibitor type 1; PAI-1; human; elastas; inhibitor; vitronectin; cell attachment; cell migration; cell proliferation; emphysema; adult respiratory distress syndrome; acute lung inflammation; alpha 1-antitrypsin deficiency; accute lung inflammation; alpha 1-antitrypsin deficiency; cystic fibrosis; atopic dermatitis; pancreatitis; periodontal disease; arthritis; HIV; atherosclerosis; restenosis; neointima; fibrosis; wound healing; tumour; metastasis; psoriasis;
                                                                                                                                                                Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                AAW26714 standard; Protein; 379
              Lawrence DA,
                                                                12-APR-1996;
                                                                                        11-APR-1997;
                                                                                                                 23-OCT-1997
                                                                                                                                          W09739028-A1
                                                                                                                                                                                                                                                                                                                      Plasminogen activator inhibitor mutant P4Ala (V343A).
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                                    (AMNA-) AMERICAN NAT RED CROSS
                                                                                                                                                                                                       thrombosis; angiogenesis; therapy.
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              Stefansson SP;
                                                                96US-0015299.
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AAU04931
AAU04932
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AAW26710
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Best Local
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           Plasminogen activator inhibitor type 1; PAI-1; human; elastase; inhibitor; vitronectin; cell attachment; cell migration; cell proliferation; emphysema; adult respiratory distress syndrome; acute lung inflammation; alpha 1-antitrypsin deficiency; cystic fibrosis; atopic dermatitis; pancreatitis; periodontal disease; arthritis; HIV; atherosclerosis; restenosis; neointima; fibrosis; wound healing; tumour; metastasis; psoriasis;
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                                                                                                                                                                                                                                                                                                    AAW26715 standard;
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                                                                                                                                                                             activator inhibitor mutant P4Asp (V343D).
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RESULT AAW26716

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Query Match Best Local S Matches

Similarity

100 0,

Score 55; DB 18; Pred. No. 0.022; 0; Mismatches 0;

0;

0 Gaps

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Length 379;

Conservative

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CC thuman plasminogen activator inhibitor (PAI-1) mature protein (see also AAWAJ587). It has an Asp for Val substitution at amino acid cresidue 343, i.e. in the reactive centre loop of the protein. The mutant can be obtained by site-directed mutagenesis of PAI-1 DNA (see AAF97303) and expression in a host cell. Claimed PAI-1 mutants (see AAW26710-25) have at least one amino acid substitution at a stabilising mutations comprising between one and cfour of His-150, Thr-154, Leu-319 and Leu-91. The mutants are characterised by being resistant to inactivation by elastase, plasminogen activator, plasmin, cathepsin G, chymase, gelatinases A cc and B, stromelysin and collagenase, and by having a high affinity crespiratory distress syndrome, acute lung inflammation, congenital calpha 1-antitrypsin deficiency, cystic fibrosis, atopic dermatitis, capancreatitis, periodontal disease, arthitis and HIV infection).

CC majoralion-induced proliferation (specifically in emphysema adult respiration-induced proliferation (specifically in atherosclerosis, cost-timely also inhibit vn-stimulated cell attachment, migration and/or migration-induced proliferation (specifically in atherosclerosis, cost-timely syndrome, confirmation after vascular graft restenosis, fibrosis (associated with chealing with scarring and fibrosis, stoweth/invasion of primary condition involving pathological angiogenesis (all claimed). Since they bind, they are more effective therapeutic agents. They also check and clearance of elastase (or its complex with PAI-1) and complex with PAI-1)
Sequence
                                                                                 promote uptake and clearance of elastase (or its complex with PAI-1) by receptors.

(NB. the amino acid sequence of the mutant protein was obtained by:
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Synthetic.
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                                                          (NB. the amino acid sequence of the mutant protein was obtained by adaptation of the wild-type sequence provided in Fig 4A of the
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(see AAW26710-25) have at least one amino acid substitution at position 343-350, especially at position 343 and/or 346, and may have additional stabilising mutations comprising between one and four of His-150, Thr-154, Leu-319 and Ile-354, and one or more of four of His-150, Thr-154, Leu-319 and Ile-354, and one or more of arg 333, Arg-335, Gly-313, Ile-372 and Leu-91. The mutants are characterised by being resistant to inactivation by elastase, glasminogen activator, plasmin, cathepsin 6, chymase, gelatinases a and B stromelysin and collagenase, and by having a high affinity for vitronectin (Vn) and are used, in vivo or in vitro, to inhibit pathological elastase activity (specifically in emphysema, adult respiratory distress syndrome, acute lung inflammation, congenital alpha l-antitrypsin deficiency, cystic fibrosis, atopic dermatitis, periodontal disease, arthritis and HIV infection). They also inhibit vn-stimulated cell attachment, migration and/or migration-induced proliferation (specifically in atherosclerosis, fost-station, congenital charmation, and are secondary respectively. They also inhibit vn-stimulated cell attachment, migration and/or migration-induced proliferation (specifically in atherosclerosis, fost-station of primary trauma, vascular graft restenosis, fibrosis (associated with charmation after vascular trauma, vascular graft restenosis, fibrosis (associated with charmation involving pathological angiogenesis (all claimed). Since the mutants are resistant to cleavage by the proteases to which they and clearance of elastase (or its complex with pair).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This polypeptide comprises a preferred mutant, PdGly (V943G), of human plasminogen activator inhibitor (PAI-1) mature protein (see also AAM31587). It has a Gly for Val substitution at amino acid residue 343, i.e. in the reactive centre loop of the protein. The mutant can be obtained by site-directed mutagenesis of PAI-1 DNA (see AAM97303) and expression in a host cell. Claimed PAI-1 mutants
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                                                                                  promote uptake and clearance of elastase (or its
yy receptors.
[MB. the amino acid sequence of the mutant protein was obtained by adaptation of the wild-type sequence provided in Fig 4A of the
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AAW26717
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This polypeptide comprises a preferred mutant, P4Leu (V343L), of also AAW31587). It has a Leu for Val substitution at amino acid calso AAW31587). It has a Leu for Val substitution at amino acid considue 343, i.e. in the reactive centre loop of the protein. The mutant can be obtained by site-directed mutagenesis of PAI-1 Mutants (see AAW36710-25) have at least one amino acid substitution at position 343-350, especially at position 343 and/or 346, and may have additional stabilising mutantions comprising between one and cour of His-530, Thr-154, Leu-319 and Leu-91. The mutants are characterised by being resistant to inactivation by elastiase, plasminogen activator, plasmin, cathepsin G, chymase, gelatinases A and B, stromelysin and ore plasmin, cathepsin G, chymase, gelatinases A and B, stromelysin and are used, in vivo or in vitro, to inhibit pathological elastase activity (specifically in emphysema, adult respiratory distress syndrome, acute lung inflammation, congenital
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Matches 11; Conserv
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Synthetic.
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neointima; fibrosis; wound healing;
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Pred. No. 0.022;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cell attachment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tumour; metastasis; psoriasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cell migration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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AAW26718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alpha l-antitrypsin deficiency, cystle fibrosis, atopic dermatitis, pariodontal disease, arthritis and HIV infection). They also inhibit Vn-stimulated cell attrachment, migration and/or post-angioplasty restenosis, neointima formation after vascular trauma, vascular graft restenosis, fibrosis (associated with chronic inflammation or chemotherapy, or of the lung), wound healing with scarring and fibrosis, growth/invasion of primary tumours or metastases, psoriasis, deep vein thrombosis and any condition involving pathological angiogenesis (all claimed). Since the mutants are resistant to cleavage by the proteases to which they bind, they are more effective therapeutic agents. They also promote uptake and clearance of elastase (or its complex with PAI-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                           cystic fibrosis; atopic dermatitis; pancreatitis; periodontal disease; arthritis; HIV; atherosclerosis; restenosis; neointima; fibrosis; wound healing; tumour; metastasis; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasminogen activator inhibitor type 1; PAI-1; human; elastase; inhibitor; vitronectin; cell attachment; cell migration; cell proliferation; emphysema; adult respiratory distress syndrome; acute lung inflammation; alpha 1-antitrypsin deficiency;
                               Claim 4; Page -; 144pp; English.
                                                           Plasminogen activator-inhibitor type I mutant inhibits elastase has high affinity for vitronectin, for therapeutic inhibition of elastase or vitronectin-mediated cell attachment, migration etc.
                                                                                                                                                                                                                        12-APR-1996;
                                                                                                                                                                                                                                                      11-APR-1997;
                                                                                                                                                                                                                                                                                                                  WO9739028-A1
                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasminogen activator inhibitor mutant P4Ile (V343I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW26718;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NB. the amino acid sequence of the mutant protein was obtained by
adaptation of the wild type sequence provided in Fig 4A of the
specification).
                                                                                                                                                           Lawrence
                                                                                                                                                                                       (AMNA-) AMERICAN NAT RED CROSS.
                                                                                                                                                                                                                                                                                    23-OCT-1997
                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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11; Conser
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nilarity 100.0
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         379 AA;
                                                                                                                                                                                                                                                                                                                                                                                               anglogenesis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                         Stefansson SP;
                                                                                                                                                                                                                        96US-0015299.
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Pred. No. 0.0
0; Mismatches
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0.022;
P4Ile (V343I),
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This polypeptide comprises a preferred

mutant,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU04922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                               Synthetic.
Homo sapie
                                                                                                                                           Key
Region
                     31-MAY-2001
                                                                    WO200138560-A2
                                                                                                                                                                                                                                                                                                          Human; Plasminogen activator inhibitor-1; PAI-1; serpin; P4Ala; immobilised enzyme; cystic fibrosis; acute respiratory distress syndrome lamobilised enzyme; cystic fibrosis; acute respiratory distress syndrome ARDS; HIV infection, Human immunodeficiency virus; prostate cancer; TRN-mediated inflammation; benign prostatic hypertrophy; mutant; mutein;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Human Plasminogen activator inhibitor-1, PAI-1, mutant P4Ala
                                                                                                                                                                                                                                                                                            V343A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU04922 standard; Protein; 379 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human plasminogen activator inhibitor (PAI-1) mature protein (see also AAW31587). It has an Ile for Val substitution at amino acid residue 343, i.e. in the reactive centre loop of the protein. The mutant can be obtained by site-directed mutagenesis of PAI-1 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           by receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NB. the amino acid sequence of the mutant protein was obtained by adaptation of the wild-type sequence provided in Fig 4A of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   346 rmapeeiimdr 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RMAPEEIIMDR 11
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                                                                                                                                                                                                                  sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
                                                                                                                  Location/Qualifiers
332 351
/label- Reactive_centre_loop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
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Pred. No. 0.022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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                                                                                                                                                                                                                                                                                                                                                                syndrome
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Note: The present sequence is not shown in the specification but is certain detection of the mature PAI-1 sequence shown in the specification but is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                              Human; Plasminogen activato
immobilised enzyme; cystic
ARDS; HIV infection; Human
TNF-mediated inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detecting a functionally active form of an enzyme in a biological sample comprises contacting an enzyme inhibitor immobilised on a solid substrate -
                                                                                                                                                                                                                                                                                                Human Plasminogen activator inhibitor-1,
                                                                                                                                                                                                                                                                                                                                                                                AAU04923;
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WO200138560-A2
                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                        26-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                     AAU04923 standard; Protein; 379 AA
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                                                       Region
                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     346 rmapeeiimdr 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RMAPEETIMDR 11
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                                                                                                                                                                                            Plasminogen activator inhibitor-1; PAI-1; serpin; P4Asp;
Lised enzyme; cystic fibrosis; acute respiratory distress syndrome;
HIV infection; Human immunodeficiency virus; prostate cancer;
diated inflammation; benign prostatic hypertrophy; mutant; mutein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nilarity 100.
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    379 AA;
                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000WO-US32315
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                                                         Location/Qualifiers 332..351
                                       /label-
                                       Reactive_centre_loop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.0%;
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Pred. No. 0.022;
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                                                                                                                                                                                                                                                                                                  PAI-1, mutant P4Asp.
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RESULT
AAU04924
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CC derived from the mature PAI-1 sequence shown in the specification but is
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                Human; Plasminogen activator inhibitor-1; PAI-1; serpin; P4Gly; immobilised enzyme; cystic fibrosis; acute respiratory distress syndrome; immobilised enzyme; cystic fibrosis; acute respiratory distress syndrome; ARDS; HIV infection; Human immunodeficiency virus; prostate cancer; TNF-mediated inflammation; benign prostatic hypertrophy; mutant; mutein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detecting a functionally active form of an enzyme in a biolo sample comprises contacting an enzyme inhibitor immobilised substrate
                                                                                                                                                                                                   Human Plasminogen activator inhibitor-1, PAI-1, mutant P4Gly.
                                                                                                                                                                                                                                                                                                    AAU04924 standard; Protein; 379 AA
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                                                                                                                                                                                                                                                                    AAU04924;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           379 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 55; ilarity 100.0%; Pred. No. Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000WO-US32315
                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                        356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 379;
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Key Region

Location/Qualifiers 332..351

Homo sapiens Synthetic

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AAU04925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence represents human plasminogen activator inhibitor-1, put ant party (73430). PAI-1 is a serine proteinase inhibitor or serpin. The protein is used to demonstrate the method of the invention which comprises detecting a functionally active form of an enzyme in a biological sample by contacting an enzyme inhibitor immobilised on a solid substrate with the biological sample and measuring the binding of the enzyme inhibitor to the active form of the enzyme by a detectable label, where the enzyme inhibitor specifically forms a covalent bond or binds with a dissociation constant of 1 x 10-9M or less with the active form of the enzyme. The present invention provides a sensitive method for the detection of a functionally active form of an enzyme in a biological sample. Human PAI-1 can be used to detect a number of enzymes including tissue plasminogen activator, urokinase, thrombin, plasmin, neutrophil elastase, pancreatic elastase, trypsin, chymotrypsin, cathepsin G and prostate specific antigen and as such can be used in methods to diagnose diseases such as cystic fibrosis, acute respiratory distress syndrome (ARDS), HIV infection, TNF-mediated inflammation, prostate cancer and benign prostatic hypertrophy.

Note: The present sequence is not shown in the specification but is
                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                            Human; Plasminogen activator inhibitor-1; PAI-1; serpin; P4Leu; immobilised enzyme; cystic fibrosis; acute respiratory distress syndrome. ARDS; HIV infection; Human immunodeficiency virus; prostate cancer; TNP-mediated inflammation; benign prostatic hypertrophy; mutant; mutein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detecting a functionally active form of an enzyme in a biological sample comprises contacting an enzyme inhibitor immobilised on a solid
                 Synthetic
                                                                                                                                                      Human Plasminogen activator inhibitor-1, PAI-1,
                                                                                                                                                                                         26-SEP-2001
                                                                                                                                                                                                                           AAU04925;
                                                                                                                                                                                                                                                            AAU04925 standard;
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                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                    100
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Pred. No.
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0.022;
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                                                                                                                                                      mutant P4Leu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 379;
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Best Local Similarity 100
Matches 11; Conservative
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Region
           Human; Plasminogen activator inhibitor-1; PAI-1; serpin; PAIle; immobilised enzyme; cystic fibrosis; acute respiratory distress syndrome; immobilised enzyme; cystic fibrosis; acute respiratory distress syndrome; ARDS; HIV infection; Human immunodeficlency virus; prostate cancer; TNF-mediated inflammation; benign prostatic hypertrophy; mutant; mutein;
                                                                                                 Human Plasminogen activator inhibitor-1, PAI-1, mutant P4Ile
                                                                                                                                      26-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                        AAU04926;
                                                                                                                                                                                                       AAU04926 standard; Protein;
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356

100. .09

Score 55; Pred. No.

DB .022; 22; 0,

Length 379;

0; Gaps

0

0,

Mismatches 0

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The sequence represents human plasminogen activator inhibitor-1, corrections of the invention of the invention of reprintant PALEU (V343L). PAI-1 is a serine proteinase inhibitor or serpin. The protein is used to demonstrate the method of the invention which comprises detecting a functionally active form of an enzyme in a cooling substrate with the biological sample and measuring the binding of the enzyme inhibitor to the active form of the enzyme by a detectable cooling substrate with the biological sample and measuring the binding of the enzyme inhibitor to the active form of the enzyme by a detectable clibids, where the enzyme inhibitor specifically forms a covalent bond or binds with a dissociation constant of 1 x 10-9M or less with the active form of the enzyme. The present invention provides a sensitive method for the detection of a functionally active form of an enzyme in a biological sample. Human pAI-1 can be used to detect a number of enzymes including tissue plasminogen activator, urokinase, thrombin, plasmin, neutrophil constate specific antigen and as such can be used in methods to diagnose (ARDS), HIV infection, TNF-mediated inflammation, prostate cancer and consider the present sequence is not shown in the specification but is constant and the present sequence is not shown in the specification but is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page - ; 69pp;
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                                                                                   derived from the mature PAI-1
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379 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English
                                                                                   sequence shown
                                                                               in the specification but shown in figure 5.
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AAR08411
                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence represents human plasminogen activator inhibitor-1, correctly the (V3431). PAI-1 is a serine proteinase inhibitor CC PAI-1, mutant P411e (V3431). PAI-1 is a serine proteinase inhibitor CC which comprises detecting a functionally active form of the invention and CC which comprises detecting a functionally active form of an enzyme in a CC solid substrate with the biological sample and measuring the binding of CC the enzyme inhibitor to the active form of the enzyme by a detectable CC label, where the enzyme inhibitor specifically forms a covalent bond or binds with a dissociation constant of 1 x 10-9M or less with the active form of the enzyme. The present invention provides a sensitive method for CC the detection of a functionally active form of an enzyme in a biological consumple. Human PAI-1 can be used to detect a number of enzymes including CC sample. Human PAI-1 can be used to detect a number of enzymes including CC tissue plasminogen activator, urokinase, thrombin, plasmin, neutrophil clastase, pancreatic elastase, trypsin, chymotrypsin, cathepsin G and prostate specific antigen and as such can be used in methods to diagnose CC diseases such as cystic fibrosis, acute respiratory distress syndrome benign prostatic hypertrophy.

Note: The present sequence is not shown in the specification but is considered from the mature PAI-1 sequence shown in figure 5.
                                                                                                                                                                                                                                                                                                                        Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 11; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page - ; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detecting a functionally active form of an enzyme in a biological sample comprises contacting an enzyme inhibitor immobilised on a solid
                Plasminogen Activator Inhibitor; fibrinolysis; liver transplants.
                                                Modified mature Plasminogen Activator Inhibitor PAI-1.
                                                                                       27-FEB-1991
                                                                                                                         AAR08411;
                                                                                                                                                            AAR08411 standard; protein; 382 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                 379 AA;
                                                                                     (first entry)
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Pred. No. 0.022;
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Best Local S
Matches 11
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See also AAQ06590-Q06594.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The N-terminal sequence of this protein can be deleted to leave SIVH or VH. The Val residue of mature PAI-1 corresponds to residue 24 of the preprotein. It may alternatively begin MVH. The protein is used in tests to identify inhibitors of its binding to tissue plasminogen activator. It is also used therapeutically to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New recombinant functional human plasminogen activator inhibitor - and plasmid expression vectors for its prodn. in E. coli, used for assays of T-PA PAI-1 inhibitors and treatment of excessive fibrinolysis
                                                W08801273-A
                                                                                                                                 Modified-site
                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                        Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Endothelial plasminogen activator inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beta plasminogen activator inhibitor encoded
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAP82007 standard; protein; 383 AA
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(29..331
                                                                                                                                                                                     label=putative glycosylation site
%55..267
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                                                                                                                                                                                                                                                                   abel- mat_beta-PAI
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Best Local Sim
Matches 11;
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                                                                                                                                                                                                            11-SEP-1987;
                                                                                                                                                                                                                                                                                                                                                Sequence of human endothelial encoded by PAI2350 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diagnostic assays for tissue - and urokinase-type plasminogen inhibitor - and pure, recombinant human endothelial plasminogen activator inhibitor.
Disclosure; ; p;
                                        Recombinant DNA coding human endothelial plasminogen activator inhibitor used for obtaining prods. having effect on blood coagulation or
                                                                                  WPI; 1988-079089/12.
N-PSDB; AAN81524.
                                                                                                                                                                                12-SEP-1986;
                                                                                                                                                                                                                                       23-MAR-1988
                                                                                                                                                                                                                                                                 EP260757-A.
                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                      Protease inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                     AAP81179;
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                                                                                                                          Pannekoek
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                                                                                                                                                    (STCL ) STICHT INSTAND BLOEDTRAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-AUG-1987;
                             ibrinolysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SCRI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1988-063992/09.
DB; AAN80253.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h 100.0%;
Similarity 100.0%;
11; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ny T,
                                                                                                                                                                                                           87EP-0201745
                                                                                                                                                                                86NL-0002307.
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 English
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                                                                                                                                                                                                                                                                                                                                                                                                                                             protein; 402 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sawdey M,
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                              plasminogen activator inhibitor (PAI)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; DB 9; I
. 0.023;
ches 0;
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RESULT
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Best Local S
Matches 11
A human umbilical cord endothelial cell cDNA library was screened with 4 oligonucleotide probes based on the known PAI-1 sequence. A 2.1kb insert was identified in the most strongly positive clones. It was inserted into pT219R to give pECE3-1 and the sequence given here. To produce mature protein, the leader sequence was removed by partial digestion with ApaLI and NS11 of HaeIII-methylase treated pECE3-1 DNA. The resulting 1800bp fragment was attached to an adaptor (to restore the first 2, Met-Val, amino acids), digested with NcoI and inserted onto NcoI-PstI cleaved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Colonies of human endothelial cDNA were screened using the probe (AANB1522) and a heterologous antiserum to detect the presence of human endothelial PAI like polypeptides. Novel recombinant DNA molecule for use in cloning and/or expressing DNA sequence in host cells which contains, in addition to a vector protein, a DNA sequence coding for human PAI is
                                                                                                                             Disclosure; Page 8; 49pp; English
                                                                                                                                                                 New recombinant functional human plasminogen activator inhibitor and plasmid expression vectors for its prodn. in E. coli, used for assays of T-PA PAI-1 inhibitors and treatment of excessive
                                                                                                                                                                                                                      WPI; 1990-361483/48
N-PSDB; AAQ06594.
                                                                                                                                                                                                                                                        Davis GL, Knabb RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
Peptide
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                                                                                                                                                                                                                                                                                                                                    08-MAY-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR07986;
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                                                                                                                                                                                                                                                                                  (DUPO) DU
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                                                                                                                                                       fibrinolysis
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11; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Activator Inhibitor PAI-1 encoded by clone ECE3-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                           89US-0350264.
                                                                                                                                                                                                                                                                                                                                    90WO-US02452
                                                                                                                                                                                                                                                                                                                                                                                                              /label- mature PAI-1
/note= "Met residue present as
PAI-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= leader peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                           residue #1 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         liver transplants
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AAW31587
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Best Local S
Matches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          elastase inhibitor; vitronectin; cell attachment; cell migration; cell proliferation; emphysema; adult respiratory distress syndrome; acute lung inflammation; alpha l-antitrypsin deficiency; cystic fibrosis; atopic dermatitis; pancreatitis; periodontal disease; arthritis; HIV; atherosclerosis; restenosis; neolntima; fibrosis; wound healing; tumour; metastasis; psoriasis; thrombosis; angiogenesis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pKK233-2 to give plasmid ptAC-PAI. This expresses mature PAI-1 with the N-terminus Val-His-His which is useful in tests to identify inhibitors of its binding to tisse plasminogen activator. The protein is also used therapeutically to treat excessive or inappropriate fibrinolysis, e.g. during liver transplant surgery. See also AAQ06590-Q06593.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasminogen activator inhibitor type 1; PAI-1; human; elastase inhibitor; vitronectin; cell attachment; cel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW31587;
                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                            Misc-difference 177
                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human plasminogen activator inhibitor type 1.
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23-OCT-1997
                                                                                              Misc-difference
                                                                                                                                                               Misc-difference 369
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                               W09739028-A1
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ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                /note-
173
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                                                                                                                           /label P1
/note pre
                                                                                              377
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                                                                                                                                                                                                                                                                               342
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Sig_peptide 24..402
                                                                                                                                                                          /label= P4
/note= "preferred substitution site
elastase inhibitor mutant"
                                                                               /note-
                                                                                                                                                                                                                                                                                                                                                                 /note-
                                                                                                                                                                                                                                                                                                                                                                                                                              /label= Mat_protein
/note= "Claim 3"
                                                                                                                                                                                                                                                               /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                               /note-
                                                             "preferred substitution site substitution"
                                                                                                                                                                                                                                              "preferred substitution site stabilisation"
                                                                                                                                                                                                                                                                                              "preferred substitution site for stabilisation"
                                                                                                                                                                                                                                                                                                                                              "preferred subsitution site for stabilisation"
                                                                                                                                                                                                                                                                                                                                                                                                "reactive centre loop region"
                                                                                                             preferred substitution site elastase inhibitor mutant"
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Pred. No. 0.024;
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Search completed: March 18, 2002, 09:48:55 Job time: 364 sec

Gaps

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Best Local S
Matches 11
                                                                                                                                                                                  This polypeptide sequence comprises wild-type human plasminogen activator inhibitor type (PAI-1). Novel mutants (see AAW26710-25) c the PAI-1 mature protein are claimed that inhibit elastase or other elastase-like proteases, or are inhibitors of vitronectin-dependent cell migration. The mutants are obtained by site-directed mutagenesis of the PAI-1 DNA sequence (see AAT97303) and expression in host cells, and have a range of therapeutic uses. Preferred mutants have amino acid substitutions in the reactive centre loop region (especially at position 343 and/or 346 of the mature protein), and may have additional stabilising amino acid substitutions at 1-4 of residues 150, 154, 319 and 354, and 1-5 of residues 333, 335, 331, 372 and 91.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasminogen activator-inhibitor type I mutant inhibits elastase has high affinity for vitronectin, for therapeutic inhibition of elastase or vitronectin-mediated cell attachment, migration etc.
                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Fig 4A; 144pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-APR-1996;
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                                                                                                                                                     Sequence
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369 rmapeelimdr 379
                 1 RMAPEEIIMDR 11
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DB; AAT97303.
                                                        Similarity 100.0%; Score 55; DB 18
Similarity 100.0%; Pred. No. 0.024;
11; Conservative 0; Mismatcher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AMERICAN NAT RED CROSS.
                                                                                                                                                     402 AA;
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                                                                                                  DB 18; Length 402;
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or

of.

Title: Perfect score: Sequence:

US-09-544-665-2 55 1 RMAPEEIIMDR 11

RMAPEEIIMDR 11

Run on: OM protein -

protein search, using sw model

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

Scoring table:

Gapop 10.0 , BLOSUM62

Gapext 0.5

Minimum DB Maximum DB

seq

length: 0 length: 2000000000

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Issued\_Patents\_AA: \*

/cgn2\_6/ptodata/2/1aa/5A\_COMB.pep:\*
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/cgn2\_6/ptodata/2/1aa/6B\_COMB.pep:\*
/cgn2\_6/ptodata/2/1aa/bcTUS\_COMB.pep:\*

of hits satisfying chosen parameters:

212252 seqs, 22503292 residues

Result

Match

Length

DB

Description

SUMMARIES

Query

100.0 100.0 100.

Sequence

444606644

390 4022 4022 4023 333 333 375 2216 4471 1166 4471 1166

pred. No. is t is

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No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution.
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                                                                                                                            COUNTRY USA
COUNTRY USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ORERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, V(
CURRENT APPLICATION UNBER: US/08/840,204
FILING DATE:
APPLICATION INFORMATION:
APPLICATION INFORMATION:
NAME: LIVANT, SHMUEL
REGISTRATION NUMBER: 33.949
REFERENCE/DOCKET NUMBER: 33.949
REFERENCE/DO
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В
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US-08-840-204-3
                                                                      Query Match
Best Local S
Matches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application Patent No. 6103498
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: LAWRENCE, DANIEL A.
APPLICANT: STEPANSSON, STEINGRHUR P.
TITLE OF INVENTION: MUTANT PLASMINOGEN ACTIVATOR-INHIBITOR
TITLE OF INVENTION: TYPE 1 (PAI-1) AND USES THEREOF
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
  346 RMAPEEIIMDR 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 2000 PEN:
CITY: WASHINGTON
STATE: DC
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                    1 RMAPEEIIMDR 11
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5, 6103498
                                                                      l Similarity
11; Conserv
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                                                                      100.0%;
ilarity 100.0%;
Conservative 0
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US-09-232-197-63
US-09-232-197-049-5
US-08-677-049-5
US-08-959-011-3
US-09-232-197-9
US-09-232-197-95
US-09-232-197-95
US-09-232-197-35
US-09-232-200-45
US-09-232-200-45
US-09-232-200-71
US-09-232-200-71
US-09-232-197-42
US-09-232-197-45
US-09-232-197-42
US-09-232-197-42
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                                                                                             Score 55; DB 3;
Pred. No. 0.008;
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                                                                          Mismatches
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                                                                                                             DB 3;
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                                                                                                         Length 379;
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Sequence
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08-121-714-6

DDRESSEE:

225 Franklin Street

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; TOPOLOGY: linear US-08-121-714-6
                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 536
PRIOR APPLICATION UMBER: 07/938
APPLICATION NUMBER: 07/938
FILING DATE: 09/01/92
APPLICATION NUMBER: 07/844
FILING DATE: 02/28/91
APPLICATION NUMBER: 07/662
APPLICATION NUMBER: 07/662
APPLICATION NUMBER: 07/662
APPLICATION NUMBER: 02/28/91
ATTORNEY/AGENT INFORMATION:
                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: 3.5* D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       uence 6, Application US/08121714
ent No. 5470970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                       369 RMAPEELIMDR 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PS/2 Model 50Z or 55SX OPERATING SYSTEM: MS-DOS (Version 5.0) SOFTWARE: WordPerfect (Version 5.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                       1 RMAPEEIIMDR 11
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                                                LE OF INVENTION: MASPIN, A NOVEL SERPIN WITH LE OF INVENTION: TUMOR SUPPRESSING ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION:
                                                                                                                                                              6, Application US/08477108A
5, 5801001
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                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fish & Richardson
Fish & Richardson P.C
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                                                                                                                                                                                                                                                                                                                                                              Score 55; DB 1; Length 390; Pred. No. 0.0083;
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Best Local :
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                equence 6, Application US/08477112 tent No. 5905023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 08
APPLICATION NUMBER: 09/01/93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" DI
                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" D1
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                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         369 RMAPEEIIMDR 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                       UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                     PPLICANT: Sager, Ruth
ITLE OF INVENTION: MASPIN, A NOVEL SERPIN WITH
ITLE OF INVENTION: TUMOR SUPPRESSING ACTIVITY
                      COMPUTER: 15M PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordberfect (Version 5.1) .
RRENT APPLICATION DATA:
APPLICATION TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAGE NO. 0.008; Score 55; DB 1; Length 390; Local Similarity 100.0%; Pred. No. 0.0083; No. 11; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 06:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 07/938.823
FILING DATE: 09/01/92
APPLICATION NUMBER: 07/844.296
FILING DATE: 02/28/92
APPLICATION NUMBER: 07/662,216
ETITING DATE: 02/28/91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/477,108A FILING DATE: June 7, 1995 CLASSIFICATION: 536
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REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ECOMMUNICATION INFORMATION: ELEPHONE: (617) 542-5070
                                                                                                                                                              OUNTRY:
                                                                                                                                                                                                                                                                                                                                              INFORMATION:
                CATION NUMBER:
                                                                                                                                             02110-2804
                                                                                                                                                                                              Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                              Massachusetts
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                                                                                                                                                                                                            E: Fish & Richardson P.C.
225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (617) 542-8906
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50z or 55SX
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0; Gaps

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TELEFAX:

US-08-477-108A-6

Matches

CLASSIFICATION: 536 IOR APPLICATION DATA:

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RESULT 5
PCT-US93-08322-6
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Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/938,823
FILING DATE: 09/01/92
APPLICATION NUMBER: 07/844,296
FILING DATE: 02/28/92
APPLICATION NUMBER: 07/662,216
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FILING DATE: 09/01/93
APPLICATION NUMBER: 07/938
FILING DATE: 09/01/92
APPLICATION NUMBER: 07/844
FILING DATE: 02/28/92
APPLICATION NUMBER: 07/662
FILING DATE: 02/28/91
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0
SOFTWARE: Wordberfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FORMATION FOR SEQ ID NO:
FILING DATE: 02/28/91
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 0530/072001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
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LENGTH: 390
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REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 06:
PELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US93/08322
                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
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Pred. No. 0.0083;
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; TOPOLOGY: 11; MOLECULE TYPE: US-08-315-461-7
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Best Local Similarity
Matches 11; Conserv
Matches
           Query Match
Best Local Similarity
                                                                                                                                                                        TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 7:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/315,461
FILING DATE: Concurrently Herewith
                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acid
                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                        CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Peptide Mediated Enhancement Of TITLE OF INVENTION: Thrombolysis: Methods and Compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     369 RMAPEETIMDR 379
                                                                                                             LENGTH: 402 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                NAME: Parker, David L.
REGISTRATION NUMBER: 32
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Houston
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Shore, Joseph D
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Conservative
                                                                                               ss: single
linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aniel T. Eitzman
                                                                                    protein
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           100.0%;
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0;
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Pred. No.
           Score 55; DB 1;
Pred. No. 0.0085;
Mismatches
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                            Length 402;
Indels
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1 RMAPEEIIMDR 11

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                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                          Sequence 2, Application US/08840204 Patent No. 6103498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-948-997-4
                                                                                                                                                                                                           GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
      STREET: 2000 - CITY: WASHINGTON STATE: DC
                                                                                                                          APPLICANT: STEFANSSON, STEINGRIMUR P.
PITLE OF INVENTION: MUTANT PLASMINGEN ACTIVATOR-INHIBITOR
FITLE OF INVENTION: TYPE 1 (PAI-1) AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: BRAIN-ASSOCIATED INHIBITOR OF TITLE OF INVENTION: TISSUE-TYPE PLASMINOGEN ACTIVATOR UMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPLICANT: HASTINGS, GREGG PPLICANT: COLEMAN, TIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/948,997
FILING DATE: Oct-10-97
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 9410 KEY WEST AVENUE CITY: ROCKVILLE STATE: MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: A. ANDERS BROOKES
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF
LECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U
                                                                            ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 55; DB 3; Length 402; ilarity 100.0%; Pred. No. 0.0085; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HUMAN GENOME SCIENCES, INC.
                                                                            MORRISON & FOERSER
                                                          PENNSYLVANIA AVENUE, NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF336
                                                                                                                                                                                                                                                                                                                                                                                                                0;
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RESULT 10
US-09-026-408-3
; Sequence 3, Application US/09026408
; Patent No. 6303338
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; LENGTH: 402
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-348-817A-4
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Best Local Sin
Matches 11;
                                                                    Query Match 100.
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn Ver
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/09348817A Patent No. 6191260
                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/348,817A CURRENT FILING DATE: 1999-07-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (202) 822-0168
TELEX: 90-4030 MRSNFOERSWSH
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 08/
PRIOR FILING DATE: 1997-10-10
PRIOR APPLICATION NUMBER: 60/
                                                                                                                                                                                                                                                                                      PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/840,20
                                                                                                                                                                                                                                                                                                                                                                                                                  TLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LIVNAT, SHMUEL
REGISTRATION NUMBER: 33,949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
369 RMAPEEIIMDR 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 402 amino acids TYPE: amino acid TOPOLOGY: linear
                                    1 RMAPEEIIMDR 11
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                                                                                                                                                                                                                                                                                                                                                                                                                               Hastings et al.
VENTION: Brain-Associated Inhibitor of Tissue-Type Plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                  PF336D1
                                                                                                                                                                                                                                                                                        1996-10-11
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100.0%; Pred. No. 0.0085;
tive 0; Mismatches 0
                                                                                          100.0%; Score 55; DB 4; 100.0%; Pred. No. 0.0085
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                                                                            Mismatches
                                                                                                            Length 402;
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                                                                            Indels
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-026-408-3
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                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/08781020 Patent No. 5792749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/934,011
FILING DATE: 15-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,056
FILING DATE: 16-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20005-332.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
PC-DOS/MS-DOS
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: WHITHAM, CURTIS, WHITHAM & MCGINN
STREET: Reston Intl. Center, 11800 Sunrise Valley Dr.,
STREET: Suite 900
                                                                                                                                                                                                                                            APPLICANT: Wright, H. TITLE OF INVENTION: M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   369 RMAPEEIIMDR 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 NEW YORK AVENUE, SUITE 600 CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: Herew
                                                             COUNTRY: 0
ZIP: 20191
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: VA
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                                                                                 USA
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                                                                                                                                                                                                                                            METHOD AND COMPOSITION FOR LOWERING LOW DENSITY LIPOPROTEIN CHOLESTEROL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PANCREAS-DERIVED PLASMINOGEN ACTIVATOR
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RESULT 13
US-08-041-774-3
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                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2
SEQ ID NO 6
LENGTH: 33
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Sequence 3, Application US/08041774
Patent No. 5550114
GENERAL INFORMATION:
APPLICANT: Strayer, David S.
TITLE OF INVENTION: EPIDERMAL GI
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                     Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/038,935
CURRENT FILING DATE: 1998-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Janciauskiene, Sabina
TITLE OF INVENTION: METHOD AND COMPOSITION FOR LOWERING LOW DENSITY
TITLE OF INVENTION: LIPOPROTEIN CHOLESTEROL
FILE REFERENCE: 294022ba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER APPLICATION NUMBER: 08/
EARLIER FILING DATE: 1997-01-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wright, H. Tonie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 09-JAN-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-391-2510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Whitham, Michael E. REGISTRATION NUMBER: 32,635 REFERENCE/DOCKET NUMBER: VCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                    1 MAPEEIIMDR 10
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5. 6150332
                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                           100.0%;
                       David S. EPIDERMAL GROWTH FACTOR INHIBITOR
                                                                                                                                                                                                                                                                         90.9%; Score 50; 100.0%; Pred. No.
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                                                                                                                                                                                                                                                           Indels
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16 LAPPEVVMD 24

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; OTHER INFORMATION: Description of Artificial Sequence: An epidermal
; OTHER INFORMATION: growth factor inhibitor peptide
US-08-530-340-2
                                                                                                                                                                               SOUTHWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: Protein
HYPOTHETICAL: N
ANTI-SENSE: N
FRAGMENT TYPE: internal
US-08-041-774-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 55...
Conservative
                                                 Query Match
Best Local Similarity 55.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2IP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CORRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/08/530,340A CURRENT FILING DATE: 1995-12-22 NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                            equence 2, Application US/08530340A atent No. 6255452
                                                                                                                                                                                                                                                                                                                                                                                                                             08-530-340-2
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INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                            PPLICANT: Strayer, David S
ITLE OF INVENTION: Epidermal Growth Factor Inhibitor
ILE REFERENCE: JEFF-0226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 LAPPEVVMD 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (212) 977-9550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTORNEY/AGENT INFORMATION:
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ZIP: 10112
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2 MAPEEIIMD 10
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REGISTRATION NUMBER: 25,385
REFERENCE/DOCKET NUMBER: 25
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T: 30 Rockefeller Plaza
New York
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                                               Score 34; DB 4; Pred. No. 5.2; 3; Mismatches
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; ANTI-SENSE: N
; FRAGMENT TYPE:
US-08-041-774-5
Search completed: March 18, 2002, 09:49:40 Job time: 224 sec
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Best Local Similarity 55.0
Matches 5; Conservative
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (212) 977-9809
TELEX: 422523 COOP UI
INFORMATION FOR SEG ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 216 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.24
CURRENT APPLICATION DATA;
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MOLECULE TYPE: |
HYPOTHETICAL: N
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MEDIUM TYPE: Floppy
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ADDRESSEE: COOPER 6 DUNHAM
STREET: 30 ROCKefeller Plaza
CITY: New York
STATE: New York
                                                                                   182 LAPPEVVMD 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Zivin, No. 555011
REGISTRATION NUMBER: 25
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: UPPILING DATE: 19930402 CLASSIFICATION: 514
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probable protein f	probable membrane	hypothetical prote	hypothetical prote	probable aminotran	cystathionine beta	hypothetical prote	pir7b protein - ri	hypothetical prote	DNA-binding respon	hypothetical prote	3',5'-cyclic-AMP p	DNA mismatch repai	STU2 protein · yea	glutaminyl-tRNA sy	hypothetical prote

## ALIGNMENTS

C;Accession: JC4265 (C;Accession: JC4265; MUID:96032362 A;Accession: JC4265 MUID:96032362 A;Accession: JC4265

C; Species: Mustela vison (American mink) C; Date: 19-Oct-1995 \*\*sequence\_revision (

08-Feb-1996 #text\_change 20-Jun-2000

plasminogen activator inhibitor type 1 precursor - American mink

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plasminogen activator inhibitor 1 precursor [validated] - human N;Alternate names; plasminogen activator inhibitor, endothelial C;Species: Homo sapiens (man) C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 08-Dec-2000 C;Accession: A28107; S02551; A26996; I59126; J50397; A25693; A26146; A29100; A25895; C;Accession: A28107; S02551; A26996; I59126; J50397; A25693; A26146; A29100; A25895; R;Bosma, P.J.; Van den Berg, E.A.; Kooistra, T.; Siemieniak, D.R.; Slightom, J.L. J. Biol. Chem. 263, 9129-9141, 1988
J.Title: Human plasminogen activator inhibitor-1 gene. Promoter and structural gene A;Reference number; A28107; MUID:88243790
A;Accession: A28107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Superfamily: antithrombin III
C;Keywords: glycoproteain; plasminogen activator; serine proteinase inhibitor
E;1-21/Domain: signal sequence #status predicted <SIG>
F;2-400/Product; plasminogen activator inhibitor type I #status predicted
E;230,286,350/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;367/Inhibitory site: Arg (plasminogen activator) #status predicted
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A;Residues: 1-400 <CHUO-
A;Residues: 1-400 | CHUO-
A;Cross-references: EMBL:X58541; NID:gl164923; PIDN:CAA41433.1; PID:gl164924
A;Experimental source: lung CCL64 epithelial cells
C;Comment: This protein controls the activities of the plasminogen activators and
A;Molecule type: DNA
A;Residues: 1-407 <BOS>
A;Residues: 1-407 <BOS>
A;Cross-references: GB:J03764; NID:g189564; PIDN:AAA60007.1; PID:g386996
A;Cross-reference; D:, Ny, T.
Eur. J. Biochem. 176, 609-616, 1988
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A:Molecule type: mRNA
A:Residues: 17-402 kWUN>
A:Residues: 17-402 kWUN>
A:Cross-references: GB:X04744; NID:g35275; PIDN:CAA28444.1; PID:g755747
A:NOte: part of this sequence, including the amino end of the mature pro R:Ny, T.; Sawdey, M.; Lawrence, D.; Millan, J.L.; Loskutoff, D.J.
Proc. Natl. Acad. Sci. U.S.A. 83, 6776-6780, 1986
A;Title: Cloning and sequence of a cDNA coding for the human beta-migral A;Reference number: A25895; MUID:86313660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:X04429; NID:g35271; PIDN:CAA28025.1; PID:g35272 R;Ginsburg, D.; Zeheb, R.; Yang, A.Y.; Rafferty, U.M.; Andreasen, P.A.; Nielsen, L.; D. J. Clin. Invest. 78, 1673-1680, 1986 A;Title: cDNA clonfing of human plasminogen activator-inhibitor from endothelial cells. A;Reference number: A92766; MUID:87058123 A;Accession: A26146
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R;Follo, M.; Ginsburg, D.
Gene 84, 447-453, 1989
A;Title: Structure and expression of the human
A;Reference number: JS0397; MUID:90128289
A;Accession: JS0397
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A;Note: the complete translation is not annotated in GenBank entries HSPAII1, HSPAII2, HR;LOSKULOFF, D.J.; Linders, M.; Keijer, J.; Veerman, H.; van Heerikhuizen, H.; Pannekoek Biochemistry 26, 3763-3768, 1987
A;Title: Structure of the human plasminogen activator inhibitor 1 gene: nonrandom distri A;Reference number: A26996; MUID:88000586
A;Title: Plasminogen activator inhibitor type-1:
A;Reference number: A91371; MUID:87080762
A;Accession: A25651
A;Molecule type: mRNA
                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 20-402 <NYT>
A; Cross references: GB:M14083;
R; Andreasen, P.A.; Riccio, A.;
FEBS Lett. 209, 213-218, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R:Wun, T.C.; Kretzmer, K.K.
FEBS Lett. 210, 11-16, 1987
A;Title: CDNA cloning and expression in E.
A;Reference number: A29100; MUID:87105925
A;Accession: A29100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;;Molecule type: DNA
;;Residues: 85-86;88-93;166-171;231-236;298-302;331-336;360-365;388-393 <FOL>
;Cross references: GB:M33156; NID:9189543
;Cross references of the intron/exon boundaries are shown
;Note: sequences of the intron/exon boundaries are shown
;Pannekoek, H.; Veerman, H.; Lambers, H.; Diergaarde, P.; Verweij, C.L.; van Zonneveld
MBO J. 5, 2539-2544, 1986
MBO J. 5, 2539-2544, 1986
MBO J. 5, 2539-2544, 1986
MBO J. 5, 2639-2544, 1986
MBO J. 6, 2639-2544, 1986
MBO J. 7, 263
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Residues: 1-402 <GIN>
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Residues: 1-9 <ZON>
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                                                                                                                                                                                                     NID:g189566; PIDN:AAA60008.1; Welinder, K.G.; Douglas, R.;
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Sartorio, R.
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J. Cell Bi
A; Title: T
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A; Residues: 1-402 <MIM>
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A; Residues: 225-235 <LAU>
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Best Local S
Matches 11
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Accession: S06745
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R;Stroemqvist, M.; Karlsson, K.E.; Bjoerquist, P.; Andersson, J.O.; Bystroem, M.; Han Biochim. Biophys. Acta 1295, 103-109, 1996
A;Title: Characterization of the complex of plasminogen activator inhibitor type 1 wi A;Reference number: S70346; MUID:96283799
A;Status. S70346
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                                                                                                                                                                                                                                                                                                                                             plasminogen activator inhibitor-1 precursor - bovine
N;Alternate names: endothelial-ceal plasminogen activator inhibi
C;Species: Bos primigenius taurus (cattle)
C;Date: 28-Feb-1990 #sequence_revision 22-Apr-1995 #text_change
C;Accession: S06745; A35855; S01324; S10906
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A;Map position: 7921.3-7922
A;Introns: 91/1; 169/1; 234/1; 300/2; 334/1; 363/1; C;Superfamily: antithrombin III
                                                                                                                                                                                                                  R;Mimuro, J.; Sawdey, M.; Hattori, M.; Luskutoff, D.J.
nucleic Acids Res. 17, 8872, 1999
A;Title: cONA for bovine type 1 plasminogen activator inhibitor
A;Reference number: S06745; MUID:90067867
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R; Kjoller; L; Martensen, P.M.; Sottrup-Jensen, L.; Jus
Eur. J. Blochem. 241, 38-46, 1996
A; Title: Conformational changes of the reactive-centre
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A;Title: Isolation of multiple types of plasminogen activator inhibitors from vascula A;Reference number: A60436; MUID:90020174
A;Recession: A60436
                         A;Cross-references: EMBL:X16383; NID:g600; PIDN:CAA34419.1; R;Pepper, M.S.; Belin, D.; Montesano, R.; Orci, L.; Vassall: J. Cell Biol. 111, 743-755, 1990
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A; Accession: S74133
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A;Cross-references: GB:X04729;
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growth factor-beta 1 modulates basic fibroblast growth factor-i
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Pred. No. 0.0
0; Mismatches
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plasminogen activator inhibitor 1 precursor - rat C;Species; Rattus norvegicus (Norway rat) C;Date: 10-Sep-1999 #text_change 10-Sep-1999 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C;Accession: A35032; JT0490; A60581; A39120 R;Bruzdzinski, C.J.; Riordan-Johnson, M.; Nordby, E.C.; Suter, S.M.; Gelehrt J. Biol. Chem. 265, 2078-2085, 1990 A;Title: Isolation and characterization of the rat plasminogen activator in A;Reference number: A35032; MUID: 90130456
                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-402 <ZEH>
A;Residues: 1-402 <ZEH>
A;Residues: 1-402 <ZEH>
A;Residues: 1-402 <ZEH>
A;Cross-references: GB:M24067; NID:g577500; PIDN:AAA56856.1; PID:g577501
A;Cross-references: GB:M24067; NID:g577500; PIDN:AAA56856.1; PID:g577501
R;Newman, M.J.; Lane, E.A.; Iannotti, A.M.; Nugent, M.A.; Pepinsky, R.B.
Endocrinology 126, 2936-2946, 1990
A;Title: Characterization and purification of a secreted plasminogen act
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R:Zeheb, R.; Gelehrter, T.D.
Gene 73, 459-468, 1988
A;Title: Cloning and sequencing of cDNA for
A;Reference number: JT0490; MUID:89211983
A;Accession: JT0490
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                                                                                 A; Molecule type: protein A; Residues: 24-48 CKBM-A; Residues: 24-48 CKBM-A; Residues: 24-48 CKBM-A; Residues: 24-48 CKBM-A; R; Olson Jr., J.A.; Shiverick, K.T.; Ogilvie, S.; Buhi, W.C.; Raizada, Proc. Natl. Acad. Sci. U.S.A. 88, 1928-1932, 1991 A; Title: Angiotensin II induces secretion of plasminogen activator in A; Reference number: A39120; MUID:91156719 A; Recession: A39120
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A;Residues: 24-49, 'L',51-63 <KAT>
C;Comment: Three types of PAI have been identified. PAI-1 is an acid-stable glycoproteir may be the primary site of synthesis of plasma PAI.
C;Comment: This inhibitor acts as "bait" for tissue plasminogen activator, urokinase, an
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R:Katagiri, K.; Okada, K.; Hattori, H.; Yano, M.
Eur. J. Biochem. 176, 81-87, 1988
A;Title: Bovine endothelial cell plasminogen activator inhibitor. Purification and A;Reference number: S01324; MUID:88329072
                                                                                                                                                                                                                                                                                                     A; Reference number: A60581; MUID: 90276328 A; Accession: A60581
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A;Accession: A35855
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                                                      Status: preliminary
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Residues: 153-235 <PEP>
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type: protein 24-43,'G' <OLS>
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Pred. No.
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A;Status:
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A; Residues: 1·197 <LIP>
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Best Local
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preliminary
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A;Cross-references: EMBL:X07863; NID:g41618; PIDN:CAA30711.1; R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; E.A.; ROSe, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12. A;Reference number: A64720; MUID:97426617
A;Recession: A65040
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: grpE
C;Superfamily: heat shock protein grpE
F:2-197/Product: heat shock protein B25
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C;Superfamily: antithrombin III
C;Superfamily: antithrombin III
C;Reywords: glycoprotein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-402/Product: plasminogen activator inhibitor-1 #status experimental <MAT>
F;86,232,288,352/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;369/Inhibitory site: Arg (plasminogen activator) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AE000347; GB:U00096; NID:g2367142; PIDN:AAC75663.1; PID:g1788
A;Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Lipinska, B.; King, J.; Ang, D.; Georgopoulos, C. Nucleic Acids Res. 16, 7545-7562, 1988
A;Title: Sequence analysis and transcriptional regulation A;Reference number: S01240; MUID:88319942
A;Accession: S01240
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N;Alternate names: grpE protein

C;Species: Escherichia colli

C;Date: 28-Aug-1999 #sequence_revision 28-Aug-1989

C;Accession: S01240; A65040
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A; Residues: 1-197 <BLAT>
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Best Local Similarity 63.0
Matches 7; Conservative
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nes 8; Conserv
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Pred. No. 1.6;
1; Mismatches
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Burland, V.;
                                                                                                           J.D.; Rose,
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protein T23G18.18 [imported] - Arabidopsis thaliana C; Speckes: Arabidopsis thaliana (mouse-ear cures) C; Date: 02-Mar-2001 *sequence_revision 02-Mar-2001 *text_change 31-Mar-2001 C; Accession: A86217 C; Accession: A86217 R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L. Authors: Hughes, B.; Huizar, L. Accession: A86217 A; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A.; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A.; Tallon, A.; Cession: A86141; MUID:21016719 A.; Accession: A86217
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A;Title: Characterization of the murine plasma fibrinolytic system. A;Reference number: $48202; MUID:95010076
A;Accession: $48208
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C;Superfamily: heat shock protein grpE
                                                                                             A; Status: preliminary
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A;Cross-references: GB:AE005174; NID:g12517038; PIDN:AAG57724.1; GSPDB:GN00145; UWGP:Z39
A;Experimental source: strain 0157:H7, substrain EDL933
  ;Cross-references: GB:AE005172; NID:g6579201; PIDN:AAF18244.1; GSPDB:GN00141; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Prendergast, G.C.; Diamond, L.E.; Dahl, D.; Cole, M.D.
ol. Cell. Biol. 10, 125-1269, 1990
r;Title: The c-myc-regulated gene mrl encodes plasminogen activator inhibitor;Reference number: A34761; MUID:90158593
Accession: A34761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lasminogen activator inhibitor 1 homolog mr1 - mouse; Species: Mus musculus (house mouse); Date: 10-Sep-1999 *sequence_revision 10-Sep-1999 *text_change 10-Sep-1999; Accession: A34761; 548208
                                                Molecule type: DNA
Residues: 1-382 <STO>
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Best Local
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Pred. No. 3.5;
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Pred. No. 1.6;
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A;Map position: 1
                                                                                                                                                                   Matches
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k:Liebergesell, M.; Steinbuchel, A. Appl. Microbiol. Biotechnol. 38, 493-501, 1993
A:Tille: Cloning and molecular analysis of the poly(3-hydroxybutyric acid) biosynthet A:Reference number: A48376; MUID:93139750
A:Accession: E48376
                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: nucleic acid
A;Molecule type: cLIE>
A;Residues: 1-692 <LIE>
A;Cross-references: GB:S54369; NID:g298249; PIDN:AAC60431.1;
A;Note: sequence extracted from NCBI backbone (NCBIN:124660,
                                                                                                                                                                                                                                                                                                                                                                           orf5 3' to phbC - Thiocystis violacea C;Species: Thiocystis violacea C;Species: Thiocystis violacea C;Date: 19-Nov-1993 **sequence_revision 25-Apr-1997 **text_change 21-Jul-2000 C;Accession: E48376 C;Accession: E48376 R;Liebergesell, M.; Steinbuchel, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Description: catalyzes the transfer of xylose from UDP-xylose to the C;Superfamily: Arabidopsis thaliana beta-1,2-xylosyltransferase C;Keywords: glycosyltransferase
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A;Gene: xylT
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A;Molecule type: mRNA
A;Residues: 1-534 <STR>
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A;Title: Molecular cloning and functional expression of beta 1,2-xylosyltransferase (A;Reference number: Z26156
A;Recession: T52649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             beta-1,2-xylosyltransferase [validated] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 24-Oct-2000 *sequence_revision 24-Oct-2000 *text_change 02-Mar-2001
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Best Local Similarity 70.0
Matches 7; Conservative
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49 RLAPEVVILD 58
                                        1 RMAPEEIIMD 10
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                                                                              ; Score 36; DB:
; Pred. No. 60;
3; Mismatches
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Pred. No. 45;
2; Mismatches
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Pred. No.
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Mismatches
                                                                                                                         <u>ب</u>
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NCBIP:124665)
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A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaed A;Reference number: A69250; MUID:98049343
A;Accession: D69274
A;Status: preliminary: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-540 <KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AE001093; GB:AE000782; NID:g2689416; PIDN:AAB91037.1; PID:g26504
C;Superfamily: probable acyl-CoA ligase medium chain; acetate--CoA ligase homology
F;50-530/Domain: acetate--CoA ligase homology <ACL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: D69274
C;Accession: D69274
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dc.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, Fleischmann, R.D.; Querbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
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Nature 390, 364-370, 1997
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                                                                                                                                                                                                                                            :Reywords: zinc finger
;303-355/Domain: GATA-type zinc finger homology <GZF>
;306-330/Region: zinc finger GATA motif
                                                                                                                                                                                                                                                                                                             ;Cross-references: SGD:S0000842; MIPS:YER040w;Map position: 5R;Superfamily: GATA-type zinc finger homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Title: Sequence and expression of GIN3;
Reference number: S22280; MUID:92049353
Accession: S22280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ibmitted to the EMBL Data Library, December 1994
;Description: The sequence of S. cerevisiae cosmids 9379,
;Reference number: S50536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Alternate names: protein YER040w
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|Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 18-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                           Status: not compared with conceptual translation; Molecule type: DNA; Residues: 1-473,'G',475-730 <MIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minehart, P.L.; Magasanik, B.
)1. Cell. Biol. 11, 6216-6228, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cross-references: EMBL:U18796; NID:g603265; PIDN:AAB64575.1; PID:g603273; MIPS:YER040
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Species: Saccharomyces cerevisiae
:Date: 28-Jan-1995 #sequence_revision 12-May-1995 #text_change 29-Oct-1999
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Best Local
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Best Local Similarity
Matches 7; Conserv
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Residues: 1-730 <DIE>
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75.0%;
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                                                                                                                                 ; Score 35; DB; Pred. No. 99; 1; Mismatches
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Pred. No. 71;
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                                                                                                                  R;Strayer,
Am. J. Pat
                                                                                                                                                             C; Accession:
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type: protein
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C;Accession: S29529

R;Accardi, L.; Gro, M.C.; di Bonito, P.; Giorgi, C.
submitted to the EMBL Data Library, September 1992
A;Description: Toscana virus genomic L segment: molecular cloning, coding strategy a A;Accession: S29529
A;Accession: S29529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA-directed DNA polymerase (EC 2.7.7.7) - Chlorella virus CV-NY-2A C;Species: Chlorella virus CV-NY-2A C;Decies: Chlorella virus CV-NY-2A C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 11-C;Accession: B42543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Superfamily: herpesvirus DNA-directed C; Keywords: DNA binding; DNA biosynthesi C; Keywords: DNA binding; DNA biosynthesi F; 182-199/Region: exonuclease pattern B F; 288-282/Region: exonuclease pattern C F; 388-401/Region: exonuclease pattern C
                                                                                                                                                       34K epidermal growth factor inhibitor, ras-like - rabbit (fragments) C;Species: Oryctolagus cuniculus (domestic rabbit) C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 28-M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Supertamily: Gukuniemi virus KNA C; Keywords: nucleotidyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: genomic RNA
A;Residues: 1-2095 <ACC:
A;Cross-references: EMDL:X68414; NID:g62199; PIDN:CAA48478.1; PID:g62200
C;Superfamily: Uukuniemi virus RNA-directed RNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N; Contains: RNA-directed
C; Species: Toscana virus
C; Date: 22-Nov-1993 #sequ
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A; Residues: 1-913 <GRA>
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A; Title: The DNA polymerase gene from chlorella
A; Reference number: A42543; MUID:92263776
A; Accession: B42543
                    Am. J. Pathol. 142, 1141-1153, 1993
A;Title: A 34-kd protein with strong homology
A;Reference number: A56771; MUID:93235943
A;Recession: A56771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genome polyprotein - Toscana virus
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A; Status: preliminary
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Best Local S
Matches 5
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                                                                          n: A56771
D.S.; Mathew, J.
hol. 142, 1141-1153, 1993
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5; Conserv
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5; Conserv
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21-731, 1992
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                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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pred. No. 3.2e+02;
5; Mismatches 1
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Search completed: March 18, 2002, 09:50:30 Job time: 239 sec	Qy 2 MA :  Db 27 LA	Query Matc Best Local Matches	A;Residues: 1-48 <str> C;Superfamily: ras tran C;Keywords: GTP binding</str>
eted: March 19 sec	2 MAPEEIIMD 10 :    ::   27 LAPPEVVMD 35	h Similarity 5; Conser	1-48 <str> ly: ras tran: GTP binding</str>
18, 2002,		61.8%; 55.6%; vative	sforming p
09:50:30		Ouery Match 61.8%; Score 34; DB 2; Length 48; Best Local Similarity 55.6%; Pred. No. 7.4;. Matches 5; Conservative 3; Mismatches 1; Indels	A;Residues: 1-48 <str> C;Superfamily: ras transforming protein; translation elongation factor Tu homology C;Reywords: GTP binding</str>
		0; Gaps	factor
		ps 0;	Tu homology

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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length: 2000000000
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55
1 RMAPEEIIMDR 11
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STU2_YEAST
MSHI_SCHPO
PI7B_ORYSA
TY95_METJA
METC_SALTY
VD87_SCHPO
PI7B_ORYSA
METC_SALTY
RANL_BACHICK
CN3A_RAT
RPAII_TRYBB
KAD_ECOLI
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SEQUENCE
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01-OCT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PLASMINOGEN ACTIVATOR INHIBITOR-1 PRECURSOR (PAI-1) (ENDOTHELIAL PLASMINOGEN ACTIVATOR INHIBITOR) (PAI).
SERPINEI OR PAI1 OR PLANHI OR PAI-1.
SERPINEI OR PAI1 OR PLANHI OR PAI-1.
EUKBRYOTA; MetaZoa, Chordatta; Craniata; Vertebrata; Euteleostomi; Mammala; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustela.
                                                                                                                                                                                                                                                                                                                                                                              EMBL; X58541; CAA41433.1; -.
HSSP; PO1008; 1ATH.
InterPro; IPR000215; Serpin.
Pfam; PF00079; Serpin; 1.
SMART; SM00093; SERPIN; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chuang T.H., Hamilton R.T., Nilsen-Hamilton M.;

"Cloning of the mink plasminogen activator inhibitor type-1 messenge RNA: an mRNA with a short half life.";

Gene 162:303-308(1995).

"I- FUNCTION: THIS INFIBITOR ACTS AS "BAIT" FOR TISSUE PLASMINOGEN ACTLYATOR, URKNINASE, AND PROTEIN C. ITS RAPID INTERACTION WITH TPA MAY FUNCTION AS A MAJOR CONTROL POINT IN THE REGULATION OF
                                                                                                                                                                                                                                                                                                       PROSITE; PS00284; SERPIN; 1.
Serpin; Serine protease inhibitor; Plasma;
Glycoprotein; Signal.
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SIMILARITY: BELONGS TO THE SERPIN FAMILY.
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PLASMINGEN ACTIVATOR INHIBITOR-1.

REACTIVE BOND (BY SIMILARITY).

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N-LINKED (GLCNAC...) (POTENTIAL).

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YEZ9_YEAST
MSHL_YEAST
MSHL_YEAST
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p3780 escherichia
p40682 bos taurus
g0sy13 thermotoga
p39956 saccharomyc
p25846 saccharomyc
p29398 thermotoga
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDILINE-90067867; PubMed-2587231;
MIDULO J., Sawdey M., Hattori M., Loskutoff D.J.;
Minuro J., Minuro J., Loskutoff D.J.;
Minuro J., Minuro J., Loskutoff D.J.;
Minuro J., Loskutoff D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1990 (Rel. 13, Greated)
01-JAN-1990 (Rel. 13, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PLASMINOGEN ACTIVATOR INHIBITOR-1 PRECURSOR (
PLASMINOGEN ACTIVATOR INHIBITOR) (PAI).
SERPINEI OR PAII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIJIE-90338128; PubMed-1696269;
Pepper M.S., Belin D., Montesano R., Orci L., Vassalli J.-D.;
"Transforming growth factor-beta 1 modulates basic fibroblast growth factor-induced proteolytic and angiogenic properties of endothelial cells in vitro.";
J. Cell Biol. 111:743-755(1990).
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P13909;
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01-JAN-1990
20-AUG-2001
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MEDLINE-88329072; PubMed-3262060;

Katagiri K., Okada K., Hattori H., Ya

Katoyine endothelial cell plasminogen

Purification and heat activation.";

Eur. J. Biochem. 176:81-87(1988).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pec
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                         EMBL; X16383; CAA34419.1; -.
EMBL; X55906; CAA37094.1; -.
EIR; S01324; S01324.
PIR; S06745; S06745.
HSSP; P01008; IATH.
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PROSITE; PS00284; SERPIN; 1. Serpin; Serine protease inhibitor; Glycoprotein; Signal.
                                                                       Pfam; PF00079; serpin; 1.
SMART; SM00093; SERPIN; 1.
PROSITE; PS00284; SERPIN;
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                                                                                                                                                                                                    interPro;
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PAII IS INACTIVATED BY PROTEOLYTIC ATTACK OF TH MISCELLANDOUS: PAII IS INACTIVATED BY PROTEOLYTIC ATTACK OF THE UROKINASE-TYPE (U-PA) AND THE TISSUE-TYPE (TPA), CLEAVING THE 369(R)-370(M) BOND.
MISCELLANDOUS: VASCULAR ENDOTHELIAL CELLS MAY BE THE PRIMARY SOF SYNTHESIS OF PLASMA PAI.
SIMILARITY: BELONGS TO THE SERPIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ... IN VILTO.";
... 111:743-755(1990).
2011 Biol. 111:743-755(1990).
FUNCTION: THIS INHIBITOR ACTS AS "BAIT" FOR TISSUE PLASMINOGEN
ACTIVATOR, UROKINASE, AND PROTEIN C. ITS RAPID INTERACTION WITH
ACTIVATOR, UROKINASE, AND PROTECTION THE REGULATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a ween the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics institute. There are no restrice by non-profit institutions as long as its content is its day this statement is not removed. Usage by and this statement is not removed. Usage by and the step in the statement is contact in the statement is not removed. Usage by and the statement is not removed. Usage by and the statement is not removed.
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CONFLICT
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CARBOHYD
CARBOHYD
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"CDNA cloning of human plasminogen activator-inhibitor from endothelial cells.";
J. Clin. Invest. 78:1673-1680(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-AUG-1987 (Rel. 05, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PLASMINOGEN ACTIVATOR INHIBITOR-1 PRECURSOR (
PLASMINOGEN ACTIVATOR INHIBITOR) (PAI).
SERPINE1 OR PAI1 OR PLANH1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-88000586; PubMed-2820474;
LOSKNtoff D.J., Linders M., Keijer J.,
van Heerikhuizen H., Pannekoek H.;
"Structure of the human plasminogen act
nonrandom distribution of introns.";
Biochemistry 26:3763-3768(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-87053819; PubMed-2430793;
MEDLINE-87053819; PubMed-2430793;
Pannekock H., Veerman H., Lambers H., Diergaa
van Zonneveld A.-J., van Mourik J.A.;
"Endothelial plasminogen activator inhibitor
the Serpin gene family.";
EMBO J. 5:2539-2544(1986).
                                                                                                                                                                                   Gene
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HUMAN
                                                                SEQUENCE FROM N.A. MEDLINE-89005111; PubMed=3262512; MEDLINE-89005111; PubMed=3262512; Strandberg L., Lawrence D., Ny T.; Strandberg L., Lawrence D., Ny T.; "The organization of the human plasminogen-activator-inhibitor-1 gene. Implications on the evolution of the serine-protease inhib
                                                                                                                                                                                                        "Structure and expression of the human activator inhibitor, PAI-1."; Gene 84:447-453(1989).
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MEDLINE-90128289; PubMed-2612914
Follo M., Ginsburg D.;
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P05121;
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                       Biochem. 176:609-616(1988)
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REACTIVE BOND.
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N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
S-> L (IN REF. 2)
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SEQUENCE FROM N.A.
MEDLINE-88243799; PubMed-3132455;
Van den Berg E.A., Kooistra T.,

Siemieniak D.R.

Promoter and

Bosma P.J., van den Slightom J.L.;

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Biol.

Chem. gene

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urokinase-type plasminogen
advanced ovarian cancer.";

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SEQUENCE OF 20-402 FROM N.A.

MEDILINE-86313660; PubMed-3092219;

NY T., Sawdey M., Lawrence D., Millan J.L., Loskutoff D.J.;

"Cloning and sequence of a cDNA coding for the human beta-migrating endothelial cell-type plasminogen activator inhibitor.";

Proc. Natl. Acad. Sci. U.S.A. 83:6776-6780(1986).
                                                                                        X-RAY CRYSTALLOGRAPHY (2.99 ANGSTROMS).
MEDLINE-99148119; PubMed-10368279;
MEDLINE-99148119; PubMed-10368279;
MEDLINE-99148119; PubMed-10368279;
Ginsburg D., Lawrence D.A., Read R.J.;
"The active conformation of plasminogen activator target for drugs to control fibrinolysis and cell structure 7:111-118(1999).
                                                                                                                                                                                                                                                                             "Interfering with the inhibitory mechanism of serpins: crystal structure of a complex formed between cleaved plasminogen activator inhibitor type 1 and a reactive-centre loop peptide."; structure 6:627-636(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).

MEDLINE-96003732; PubMed-7552714;

Aertgeerts K., de Bondt H.L., de Ranter C.J., Declerck P.J.;

Mechanisms contributing to the conformational and functional
flaxibility of plasminogen activator inhibitor-1.";

Nat. Struct. Biol. 2:891-897(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
MEDLINE-92114970; PubMed-1731226;
Mottonen J., Strand A., Symersky J., Sweet R.M.,
Geoghegan K.F., Gerard R.D., Goldsmith E.J.;
"Structural basis of latency in plasminogen activ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDILINE-87080762; PubMed=3025016;
Andreasen P.A., Riccio A., Welinder K.G., Douglas R., Sartorio R.,
Nielsen L.S., Oppenheimer C., Blasi F., Dance K.;
"Plasminogen activator inhibitor type-1: reactive center and amino-
terminal heterogeneity determined by protein and cDNA sequencing.";
FEBS Lett. 209:213-218(1986).
VARÎANT THR-15.
MEDLINE-97337920; PubMed-9194591;
Turkmen B., Schmitt M., Schmalfeldt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nun T.C., Kretzmer K.K.;

*CDNA cloning and expression

inhibitor (PAI) related to a

FEBS Lett. 210:11-16(1987).
                                                                                                                                                                                                                                                                                                                                                                                            Kue Y., Bjorquist
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4EDLINE-98298439; PubMed-9634700;
ue Y., Bjorquist P., Inghardt T., Linschoten
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EMBL; X13339; CAB51639.1;
EMBL; X13340; CAB51737.1;
EMBL; X13340; CAB51606.1;
EMBL; X13341; CAB51607.1;
EMBL; X13342; CAB51607.1;
EMBL; X13343; CAB51739.1;
EMBL; X13344; CAB51739.1;
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EMBL; X13344; CAA31729.1;
EMBL; X13344; CAA31729.1;
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"Mutational analysis of the genes encoding urokinase-type plasminoger
activator (uPA) and its inhibitor PAI-1 in advanced ovarian cancer."
Electrophoresis 18:686-689(1997).
-i- FUNCTION: THIS INHIBITOR ACTS AS "BAIT" FOR TISSUE PLASMINOGEN
ACTIVATOR, UROKINASE, AND PROTEIN C. ITS RAPID INTERACTION WITH
  CARBOHYD
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                                                                                                                                                                                                                              InterPro; IPR000215; S. Pfam; PF00079; serpin;
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protease inhibitor;
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  PLASMINOGEN ACTIVATOR II
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N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PLASMINOGEN ACTIVATOR INHIBITOR-1 PRECURSOR (PAI-1) (ENDOTHELIAL PLASMINOGEN ACTIVATOR INHIBITOR) (PAI).
SERPINE1 OR PAI1 OR PLANH1.
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                                                                                                                                                                                                                   Glycoprotein;
SIGNAL
                                                                                                                                                                                                                                                                                                           Pfam; PF00079; serpin; SMART; SM00093; SERPIN
                                                                                                                                                                                                                                                                                                                                                EMBL; Y11347; CAA72182.1; -. HSSP; P01008; IATH. InterPro; IPR000215; Serpin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bijnens A.P., Knockaert I., Cousin E., Kruithof E.K.O., Declerck P. Thromb. Haemost. 77:1046-1046(1997).

Thromb. Haemost. 77:1046-1046(1997).

FUNCTION: THIS INHIBITOR ACTS AS "BAIT" FOR TISSUE PLASMINOGEN -ACTIVATOR, UROKINASE, AND PROTEIN C. ITS RAPID INTERACTION WITTER MAY FUNCTION AS A MAJOR CONTROL POINT IN THE REGULATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bijnens A.P., Knockaert I., Cousin 
"Expression and characterization of 
activator inhibitor-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ERRATUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleóstomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sus scrofa (Pig).
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                                                                                                                                                                                                                                                                                   PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thromb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-97206538; PubMed-9157595;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAI1_PIG
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Similarity
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PS00284; SERPIN;
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; Pred. No. 0.0017;
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PLASMINOGEN ACTIVATOR INHIBITOR-1
Score
Pred.
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                                                                                                                                                                                                                                                             Plasma;
  S5;
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recombinant porcine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  402
  DB 1;
0.0017;
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                                                                                                                                                                                                                                                                                        SMART;
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Bruzdzinski C.J.,
Gelehrter T.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PLASMINOGEN ACTIVATOR INHIBITOR-1 PRECURSOR (PAI-1) (ENDOTHELIAL PLASMINOGEN ACTIVATOR INHIBITOR) (PAI).
SERPINE1 OR PAI1 OR PLANH1.
                                                                                                                                                                                                                                                                                   EMBL; J05206; AAA41796.1;
EMBL; M24067; AAA56856.1;
PIR; A35032; A35032.
HSSP; P01008; IATH.
                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                  Serpin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inhibitor-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zeheb R., Gelehrter T.D., "Cloning and sequencing o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zeheb R., Gelehrter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-89211983; PubMed-3149611;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Isolation and characterization of the rat plasminogen activator inhibitor-1 gene.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat)
                                                                                                                                                                                                                    InterPro; IPR000215; Serpin: 1. star; PF00079; serpin; 1. star; SM00093; SERPIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: THIS INHIBITOR ACTS AS "BAIT" FOR TISSUE PLASMINOGEN ACTIVATOR, UROKINASE, AND PROTEIN C. ITS RAPID INTERACTION WITH TPA MAY FUNCTION AS A MAJOR CONTROL POINT IN THE REGULATION OF FIBRINOLUSIS.

MISCELLANEOUS: PAI1 IS INACTIVATED BY PROTEOLYTIC ATTACK OF THE UROKINASE-TYPE (U-PA) AND THE TISSUE-TYPE (TPA), CLEAVING THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE
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32 232
88 288
52 352
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                                                                                                                                                                                  protease inhibitor; Plasma; Plasminogen
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Riordan-Johnson
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                  BY SIMILARITY.

PLASMINOGEN ACTIVATOR I

REACTIVE BOND.

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N-LINKED (GLCNAC...)

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N-LINKED (GLCNAC...)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SERPIN FAMILY
         2B639140F475EB53
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TEIN C. ITS RAPID INTERACTION WIT
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                                                               (POTENTIAL)
                                                                                                                                                                                         activation;
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01-MAR-1989 (Rel. 10, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
GRPE PROTEIN (HSP-70 COFACTOR) (HEAT SHOCK PROTEIN
GRPE OR B3614
                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-97349980; PubMed-9205837;
Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K.,
Yamamoto Y., Aiba H., Baba T., Hayashi K., Miki T., Mitsuhashi N.,
Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,
Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasundaram S.,
Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
Yamagata S., Horiuchi T.;
Yamagata S., Horiuchi T.;
*Construction of a contiguous 874-kb sequence of the Escherichia coli
*Kl2 genome corresponding to 50.0-68.8 min on the linkage map and
analysis of its sequence features.*;
DNA Res. 4:91-113(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                 POSSIBLE FUNCTION.

MEDLINE-91187894; PubMed-1826368;

Liberek K., Marszalek J., Ang D., Georgopoulos C., 2

Liberek K. Marszalek J., Ang D. Georgopoulos C., 2

"Escherichia coli Dnad and GrpE heat shock proteins

"Escherichia coli DnaK.";

Proc. Natl. Acad. Sci. U.S.A. 88:2874-2878(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lipinska B., King J., Ang D., Georgopoulos C.;
"Sequence analysis and transcriptional regulation coll grpE gene, encoding a heat shock protein.";
Nucleic Acids Res. 16:7545-7562(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GRPE_ECOLI P09372;
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x-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
MEDLINE-97258949; PubMed-9103205;
Harrison C.J., Hayer-Harri M., dl Liberto M.,
"Crystal structure of the nucleotide exchange
                                                                                                                                                                 FUNCTION, AND MUTAGENESIS.
MEDLINE-9704508); PubMed-8890154;
MU B., Wawrzynow A., Zylicz M., GG
"Structure-function analysis of to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
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Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-88319942; PubMed-3045760;
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                                                                                                                     MBO J. 15:4806-4816(1996)
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P22777;

Ol-AUG-1991 (Rel. 19, Created)
Ol AUG-1991 (Rel. 19, Last sequence update)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last sequence update)
21-AUG-2001 (Rel. 40, Last sequence update)
22-AUG-2001 (Rel. 40, Last sequence update)
23-AUG-2001 (Rel. 19, Last sequence update)
24-AUG-2001 (Rel. 19, Last sequence update)
25-AUG-2001 (Rel. 19, Last sequence update)
25-AUG-2001 (Rel. 19, Created)
27-AUG-2001 (Rel. 19, Created)
28-AUG-2001 (Rel. 19, Created)
29-AUG-2001 (Rel. 19, Created)
29-AUG-2001 (Rel. 19, Created)
20-AUG-2001 (Rel. 19, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EcoGene; EG10416; grpE.
InterPro; IPR000740; GrpE.
Pfam; PP01025; GrpE; 1.
PRINTS; PR00773; GRPEPROTEIN.
PROSTTE; PS01071; GRPE; 1.
Chaperone; Heat shock; 3D-structure; Complete SEQUENCE 197 AA; 21798 MW; CDC4CD9D0BAD4BE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-90188593; PubMed-2406566;
Prendergast G.C., Diamond L.E., Dahl D.,
"The c-myc-regulated gene mrl encodes pla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOUSE
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                                                                                                                                                                                                     FIBRINOLYSIS.

MISCELLANEOUS: PAII IS INACTIVATED BY PROTEOLYTIC ATTACK OF THE UROKINASE-TYPE (U-PA) AND THE TISSUE-TYPE (TPA), CLEAVING THE
                                                                                                                                369(R)-370(M) BOND. SIMILARITY: BELONGS TO THE SERPIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                          Cell. Biol. 10:1265-1269(1990).
FUNCTION: THIS INHIBITOR ACTS AS "BAIT" FOR TISSUE PLASMINOGEN ACTVATOR, UPOKINASE, AND PROTEIN C. ITS RAPID INTERACTION WITH TPA MAY FUNCTION AS A MAJOR CONTROL POINT IN THE REGULATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INDUCTION: BY THE SIGMA(32) SUBUNIT OF RNA POLYMERASE. SIMILARITY: BELONGS TO THE GRPE FAMILY.
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Pred. No.
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Sciurognathi; Muridae;
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P SEQUENCE OF 1-494 FROM N.A.

C STRAIN-ATCC 1908 / CB15;

X MEDIINE-98012985; pubmd-9352936;

X MEDIINE-98012985; pubmd-9352936;

X Steinman H.M., Fareed F., Weinstein L.;

T "Catalase-peroxidase of Caulobacter crescentus: function and ro

T stationary-phase survival.*;

J. Bacteriol. 179:6831-6836(1997).

J. Bacteriol. 179:6831-6836(1997)

J. Bacteriol. 179:6831-6836(1997)

G. -- FUNCTION. BIFUNCTIONAL, EXHIBITING BOTH A CATALASE AND

BROAD-SPECTRUM PEROXIDASE ACTIVITIES.

C --- CATALYTIC ACTIVITY: DONOR + H(2)O(2) - OXIDIZED DONOR + 2 H

C --- COATALYTIC ACTIVITY: DONOR + 100 SET SIMILARITY).

C --- INDUCTION: BY EXPOSURE TO HYDROGEN PEROXIDE.
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031066;
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CARBOHYD
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-ACCC 19089 / CB15;
STRAIN-ACCC 19089 / Dubmed-11259647;
Mierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
Risen J., Heidelberg J.F., Alley M.K.R., Ohta N., Maddock J.R.,
Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.
Salzberg S.L., Shapiro L., Venter J.C., Fraser C.M.;
"Complete genome sequence of Caulobacter crescentus.";
Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
PEROXIDASE/CATALASE (EC 1.11.1.6) (CATALASE-PEROXIDASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-slb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
Caulobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caulobacter crescentus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KATG OR CC3043
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Serpin; Serine protease inhibitor; Plasma; Plasminogen activation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=69394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 369 RMAPTEMVIDR 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nterPro;
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Pr00079; serpin; 1.
%; SM00093; SERPIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGI:97608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P01008; 1ATH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 63. 7; Conservative
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PR000215; Serpin
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45170 MW:
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PLASMINOGEN ACTIVATOR INHIBITOR-1.

REACTIVE BOND.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . . .) (POTENTIAL).

MW; 765FF1659C70F68C CRC64;
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; Pred. No.
3; Mismatc
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(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
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tent is in
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Best Local S
Matches 7
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EMBL; AF027168; AAC43850.1; -.
HSSP; P48514; 1APX.
TIGR; CC3044; -.
InterPro; IPR002016; Peroxidase.
InterPro; IPR002016; Peroxidase; 1.
PR0SITE; PS00435; PEROXIDASE.1; 1.
PR0SITE; PS00436; PEROXIDASE.2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P45365;
01-NOV-1995 (
01-NOV-1995 (
01-OCT-1996 )
                                                                                                                                                                                                                                  SEQUENCE FROM N. A.
STRAIN-2311 / DSM 208;
STRAIN-2511 / DSM 208;
MEDLINE-93159750; PUDMed-7763384;
Liebergesell M., Steinbuechel A.;
Liebergesell M., Steinbuechel A.;
"Cloning and molecular analysis of the poly(3-hydroxybutyric acid)
biosynthetic genes of Thiocystis violacea.";
biosynthetic genes of Thiocystis violacea.",
Appl. Microbiol. Biotechnol. 38:493-501(1993).
Appl. Microbiol. Biotechnol. 38:493-501(1993).
REGULATORY COMPONENTS OF SENSORY TRANSDUCTION SYSTEMS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete
ACT_SITE
ACT_SITE
BINDING
                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
HYPOTHETICAL 76.5 KDA PROTEIN IN PHBC 3'REGION (ORF5).
Thiocystis violacea.
Bacteria, Proteobacteria; gamma subdivision; Chromatiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced throughla collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
            EMBL; L01113; AAB02863.1; -. EMBL; S54369; AAC60431.1; -. InterPro; IPR001633; DUF2. InterPro; IPR000160; DUF9. InterPro; IPR0001789; Response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THIVI
                                                                                                                                                                                                                                                                                                                                                                                                                       Thiocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=13725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PH5_THIVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 601 MAPEEALVDR 610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; Conservative
                                                                                                            an email to license@isb-sib.ch).
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106
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106
268
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70.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
BY SIMILARITY.
PROXIMAL HEME LIGAND (BY SIMILARITY).
D900742D04E02E97 CRC64;
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Response\_reg

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Query Match
Best Local Similarity
""" 6; Conserv
       RA Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Araujo R.,
RA Chung E., Duncan M., Guzman E., Hartzell G., Hunicke-Smith S.,
RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
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RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
RA Hyman R., Kayser A., Kayser A., Rasponse To The Repucker To The Sympthems of The Northern Continuation of Glutamine C. Sympthems and Catalary Tope C., Sympthems C., Lashkari S., Rasponse To The Sympthems Contained C., Lashkari S., Rasponse To The Repucker Tope C., Sympthems C., Lashkari S., Rasponse Tope Sympthems C.
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GLIA3_YEAST STANDARD; PRT; 7
P18494;
O1-NOV-1990 (Rel. 16, Created)
O1-FEB-1995 (Rel. 31, Last sequence up
O1-FEB-1995 (Rel. 40, Last annotation)
EMBL; M35267; AAA34645.1;
EMBL; U18796; AAB64575.1;
PIR; S22280; S22280.
HSSP; P17429; 5GAT.
                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBI outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
Eukaryota: Fungi; Ascomycota: Saccharomycotina; Saccharomycetes:
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein;
MOD_RES 188 18
SEQUENCE 692 AA; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART;
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Pfam; I
SMART;
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Dietrich F.S., Mulligan J.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE-92049353; Pubmed-1682800;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomycetales;
NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Sequence and expression of GLN3, a positive nitrogen regulatory gene of Saccharomyces cerevisae encoding a protein with a putative zinc finger DNA-binding domain." a graph of Saccharomyces cerevisae encoding a protein with a putative zinc finger DNA-binding domain." a graph of Cell. Biol. 11:6216-6228(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minehart P.L., Magasanik B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |:||| :|:|
49 RLAPEVVILD 58
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m; PF00072; response reg; 1
RT; SM00267; DUF1; 1.
RT; SM00052; DUF2; 1.
RT; SM00448; REC; 1.
                                                                                                                       àn
                                                                                               requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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76476 MW;
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B PHOSPHORYLATION (BY SIMILARITY).
6476 MW; F6880E63F44E11F7 CRC64;
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Pred. No. 20;
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on update)
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Best Local S
                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Grabherr R., Strasser P., van Etten J.L.;
"The DNA polymerase gene from chlorella viruses PBCV-1 contains an intron with nuclear splicing sequences.";
virology 188:721-731(1992), POLYMERASE ACTIVITY, THIS POTENTIALLY EXTRIBITS 3' TO 5' EXONUCLEASE ACTIVITY.
-1- CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DPOL_CHVN2
P30320;
                                                                                                      PRINTS; PR00106; DNAPOLB.
SMART; SM00466; POLBC; 1.
PROSITE; PS00116; DNA_POLYMERASE_B; 1.
Transferase; DNA-directed DNA polymerase; DNA replication;
DNA-binding; Hydrolase; Nuclease; Exonuclease; Multifunctional enzyme;
                                                                                                                                                                                                                                    EMBL; M86837; AAA88827.1; -. PIR; B42543; B42543; InterPro; IPR002064; DNA_pol_B. Pfam; PF00136; DNA_pol_B; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
DNA POLYMERASE (EC 2.7.7.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nuclear protein; Nitrate assimilation CAR-FING 306 330 GARA-TYP DOMAIN 351 351 ARG/LYS-CONFLICT 474 474 P -> G (SEQUENCE 730 AA; 79382 MW; 3159E1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO0619; GATARNETINGER.
SMART; SM00401; ZnF_GATA; 1.

PROSITE; PS00344; GATA_ZN_FINGER_1; 1.

PROSITE; PS50114; GATA_ZN_FINGER_2; 1.

Transcription regulation; Activator; DNA-binding; Zinc-finger;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE-92263776; PubMed-1585643;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chlorella virus NY-2A (CV-NY2A).
Viruses; dsDNA viruses, no RNA s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHVN2
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InterPro; IPR000679;
Pfam; PF00320; GATA;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-12619;
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7; Conserv
  913 AA;
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  104955
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  MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 35; ; Pred. No. 3 1; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNA stage; Phycodnaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARG/LYS-RICH (BASIC).
P -> G (IN REF. 1).
; 3159E1844469942E CRC64;
CONTAINS CONSERVED RESIDUES ESSENTIAL 3' -> 5' EXONUCLEASE ACTIVITIES. 4; 7E656423123B02B5 CRC64;
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Best Local Similarity 45...
"---hes 5; Conservative
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01-OCT-1994
20-AUG-2001
                                                                                                                                                                                                                                             01-OCT-1993 (Rel. 27, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
MOLYBDOPTERIN-GUANINE DINUCLEOTIDE BIOSYNTHESIS PROTEIN MOBB OR B3856.
                                                                                                                                                                                                                                                                                                                                                                     MOBB_ECOLI (
P32125; P76770;
01-OCT-1993 (Re)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .1519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBI outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X68414; CAA48478.1; -. PIR; S29529; S29529.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIINE-93212587; PubMed-8460526; Acceard L., Gro M.C., di Bonito P., Giorgi C.; Tressena virus genomic L segment: molecular cloning, coding and amino acid sequence in comparison with other negative st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Toscana virus (Tos).
Viruses; ssRNA negat
NCBI_TaxID=11590;
SEQUENCE FROM N.A.
STRAIN=812 / MG1655;
MEDLINE-93347969; PubMed-8346018;
Plunkett G. III, Burland V.D., Daniels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Virus Res. 27:119-131(1993).
-I- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE - N PYROPHOSPHATE
                                                                                                                                                                                             Bacteria; Proteobacteria;
                                                                                                                                                                                                                             Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transferase; Nucleotidyltransferase; RNA-directed SEQUENCE 2095 AA; 238885 MW; 22FF4DAD745583B7
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                                                                                                                                                                          Escherichia.
                                                                                                                                       NCBI_TaxID=562;
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RVAPEKLVSDK 1529
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(Rel. 30, Last sequence update)
(Rel. 40, Last annotation update)
D RNA POLYMERASE (EC 2.7.7.48) (L
                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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Matches 5
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Q61820;
Q1-NOV-1997
Q1-NOV-1997
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GTP-BINDING
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MEDLINE-97362202; PubMed-9219527;
MEDLINE-97362202; PubMed-9219527;
MEDLINE-97362202; PubMed-9219527;
MEDLINE-97362202; PubMed-97362202; PubMe
   MEDLINE-95152168; PubMed-7849398; Coutavas E.E., Hsieh C.M., Ren M., D'Eustachio P.D.; D'Eustachio P.D.; The Medical P.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
PIR; S
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Nucleic Acids Res. 21:3391-3398(1993).
[2]
                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
MCBI_TaxID=10090;
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(Rel. 35, Last sequence update)
(Rel. 37, Last annotation updat
NUCLEAR PROTEIN RAN, TESTIS-SPE
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19232 MW;
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Sciurognathi; Muridae; Murinae; Mus
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GTP (POTENTIAL).
GTP (POTENTIAL).
C3522F4DFBF3833C (
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Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                RAN_CHICK
P42558;
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                                                                                                                                                                                                                                                                                      01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-DEC-1996 (Rel. 37, Last annotation update)
GTP-BINDING NUCLEAR PROTEIN RAN (TC4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART;
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InterPro; IPR002041; RAN.
InterPro; IPR001806; Ras_trnsfrmng.
InterPro; IPR003575; Small_GTPase.
Pfam; PF00071; ras; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L32752; AAA64248.1; -. HSSP; P28746; 1A2K.
                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-92339546; PubMed-1633874;
Trueb J., Trueb B.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PRO0449; RASTRNSFRMNG.
PRINTS; PRO0627; GTPRANTC4.
SMART; SM00176; RAN; 1.
SMART; SM00010; small_GTPase;
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les 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            216 AA;
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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
IBB (BY SIMILARITY).
IBB (BY SIMILARITY).
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Pred. No. 14;
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                                                                                                                                                  GTP-binding;
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 182 LAPPEVVMD 190
                     2 MAPEEIIMD 10
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Search completed: March 18, 2002, 09:52:25 Job time: 294 sec

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Copyright (c) 1993 - 2000 Compugen Ltd
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O91kK7 arabidopsis
O91dh0 arabidopsis
O9708 agrobacteri
O99016 paramecium
O99018 paramecium
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Q9cci6 mycobacteri
Q9ulb4 leishmania
Q9lkk7 arabidopsis
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RESULT 2
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OSSGCB;
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
T23G18.18
T23G18.18
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; core-eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID-3702;
                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AC011438; AAF18244.1; -
INTERPROJECT SET LIP thioest actsite. SEQUENCE 382 AA; 43223 MN; 353040AF91BC84E0 CRC64;
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                                                                                                                                                        345
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7; Conserv
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Database

SPTREMBL\_17:\*
1: sp\_archea:\*
2: sp\_bacteria:\*
3: sp\_fungi:\*
4: sp\_human:\*
5: sp\_invertebrat

Post-processing:

Minimum Match 0% Maximum Match 100% Listing first 45 s

summaries

Minimum

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length:

length: 2000000000

number of DB DB

Scoring table: Sequence: Title: Perfect score:

Gapop 10.0 ,

Gapext 0.5

US-09-544-665-2 55

RMAPEEIIMDR 11

Run on:

protein -

protein search, using sw model

March 18, 2002, 09:51:54;

Result No

Score

Query Match

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1382 1369 329 533 534 723 723 220 220 220 220 220 220 1493 1493 1493 120 131

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030043 0905K5 09F0L8 09P2E4 099WD1 09TS94 09A256

Pred. No. is th score greater t and is derived

6: 7: 8: 9: 110: 112: 113:

sp\_plant:\*

sp\_virus:\*
sp\_vertebrate:\*
sp\_unclassified:\*

sp\_organelle:\*
sp\_phage:\* sp\_mhc:\* sp\_mammal:\* sp\_invertebrate:\*

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Best Local Similarity 54.5
Matches 6; Conservative
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Q9U1B4;
Q9U1B4;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-MAY-2001 (TrEMBLrel. 17, Last annotation update)
POSSIBLE BETA PROPELLER PROTEIN (FRAGMENT).
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
RMBL: AL583919; CAC30290.1; -.
InterPro; IPR000309; TrkA_Kuptake.
Pfam; PP02080; TrkA; 1.
Hypothetical protein; Complete proteome.
Hypothetical protein; Complete proteome.
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Cole S.T., Eiglmeier K., Parkhill J.,
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                                                                                                                                                                                                                MEDLINE-98146435; PubMed-9477341;
Ivens A.C., Lewis S.M., Bagherzadeh A.,
Smith D.F.;
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-FRIEDLIN;
Zimmermann W., Wambutt R., I
Rajandream M.A., Barrell B.C
Submitted (DEC-1999) to the
                        "A physical map of the Leishmania major Genome Res. 8:135-145(1998).

EMBL: AL12185; Ch858300.1; ...

InterPro; IPR001680; WD40.

pfam; PF00400; WD40.3

SMART; SM0320; WD_REPEATS_REGION; 1.

PROSITE; PS50294; WD_REPEATS_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leishmania major.
Eukaryota; Eugler
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-FRIEDLIN;
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.G.;
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Best Local S
Matches 5
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Best Local S
Matches 6
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01-OCT-2000 (TrEMBLrel. 15, L
01-MAR-2001 (TrEMBLrel. 16, L
BETA1,2-XYLOSYLTRANSFERASE (G
CLONE:MTE17).
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SEQUENCE
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STRAIN-CV, WS;
GOMORD V., Baltresca V., Klefer-Meyer M.-C., Faye L.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AF272852; AAF77064.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BETA 1.2-XYLOSYLTRANSFERASE.
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; core eudicots; Rosidae;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID-3702;
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SEQUENCE 533 AA;
                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; core eudicots; Rosidae; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                   SEQUENCE FROM N.A. Bakker H.;
                                                                                                                          Steinkellner H.; "Molecular cloning and functional expression of beta wholecular cloning and from Arabidopsis thaliana."; xylosyltransferase cDNA from Arabidopsis thaliana."; FEBS Lett. 472:105-108(2000).
                                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
MEDLINE-20245450; PubMed-10781814;
MEDLINE-20245450; PubMed-10781814;
MEDLINE-20245450; PubMed-10781814;
                                                                                                                                                                                                                                                                                                                       NCBI_TaxID-3702;
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"Arabidopsis cDNA for betal,2-xylosyltransferase.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
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(GENOMIC DNA, CHROMOSOME
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Matches 6
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Best Local Similarity 50.0
Matches 5; Conservative
0990L6 PRELIMINARY;
0990L6;
01-JUN-2001 (TrEMBLrel. 17, C)
01-JUN-2001 (TrEMBLrel. 17, I)
01-JUN-2001 (TREMBLrel. 17, II)
01-JUN-2001 (TREMBLrel. 17, II)
DNA POLYMERASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9R708;
Q1-MAY-2000
Q1-MAY-2000
Q1-JUN-2001
                                                                                                                                                                                                       Pfam; PF00141; peroxidase; 1.
PRINTS; PR00458; PEROXIDASE.
PROSITE; PS00436; PEROXIDASE_2; UNKNOWN_1.
PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
SEQUENCE 723 AA; 78741 MW; AA531987F535B508 CRC64;
                                                                                                                                                                                                                                                                                                            Transferase.
534 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Structural analysis of Arabidopsis thalians chromosome 5. VII. Sequence features of the regions of 1,013,767 bp covered by sixteen physically assigned pl and TAC clones.";

DNA Res 5:297-308(1998).

EMBL; AJ77103; CAB90610.1;

EMBL; AJ77103; CAB9489.1;

EMBL; AB015479; BAB08567.1;
                                                                                                                                                                                                                                                                                                                                                                              Agrobacterium radiobacter.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9R708
                                                                                                                                                                                                                                                                                  Mol. Microbiol. 0:0-0(1999).
EMBL; AB033631; BAA89349.1; -.
HSSP; P48534; 1APX.
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SEQUENCE FROM
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                                                                                                         588 VSPEELLLDR
                                                                                                                                                                                                                                                          InterPro; IPR002016; Peroxidase.
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27 RMVPDRIVMSR 137
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S., Asamizu E., Kaneko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60234 MW;
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         Created)
Last sequence update)
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Last sequence update)
Last annotation update)
                                                                                                                                                   Score 36; DB
Pred. No. 1.8e
5; Mismatches
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                                                       PRT;
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                                                                                                                                                DB 2;
1.8e+02;
0;
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1.3e+02;
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Best Local S
Matches 5
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Best Local S
Matches 5
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Q99018;
Q1-JUN-2001
01-JUN-2001
01-JUN-2001
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF NON_TER
                                                                                                        099017, PRELIMINARY;
099017;
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TREMBLREL. 17,
Paramecium bursaria chlorella v
Viruses; dsDNA viruses, no RNA
NCBI_TaxID=10506;
[1]
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EMBL; AF344230; AAK28
NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=NY-2A;
Zhang Y., Adams B., S
"Intron conservation
viruses.";
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EMBL; AF344202; AAK28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhang Y., Adams B., & "Intron conservation viruses.";
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STRAIN-AR158;
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Paramecium bursaria chlorella virus 1 (PBCV-1).

Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae;

NCBI_TaxID=10506;
                                                                           DNA POLYMERASE (FRAGMENT).
DPO.
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Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Phycodnavirus.
NCBI_TaxID-10506;
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5; Conservative
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5; Conservative
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220 AA;
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220 AA;
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AAK28923.1;
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24945 MW;
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                                                                                                                                                                                                                                                                                                                                                    ; Score 35; DB; Pred. No. 80; 4; Mismatches
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DNA poly
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Last sequence update)
Last annotation update)
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Last annotation updat
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DNA polymerase gene encoded
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Pred. No.
                                         n virus 1
NA stage;
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polymerase gene encoded
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                                         (PBCV-1).
Phycodnaviridae;
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80;
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RESULT 11
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ID 030043
AC 030043
DT 01-JAN
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Best Local S
Matches 5
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Best Local
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Q99013;
01-JUN-2001
01-JUN-2001
01-JUN-2001
                                                                                                                                                                                           O30043 PRELIMINARY; PRT; 240 AA.
C)30043;
O1-JAN-1998 (TrEMBLrel. 05, Created)
O1-JAN-1998 (TrEMBLrel. 05, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MEDIUM-CHAIN ACYL-COA LIGASE (ALKK-1).
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NON_TER
SEQUENCE
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SEQUENCE FROM N.A.
STRAIN-WC-16 / DSM 4304 / ATCC 49558;
STRAINE-B0409343; PubMed-9389475;
Klenk H.-P., Clayton R.A., Tomb J.-F.
                                                                                                                       Archaeoglobus fulgidus.
Archaea; Euryarchaeota;
Archaeoglobus.
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"Intron conservation viruses.":
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STRAIN-NYS-1;
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Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Phycodnavirus
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STRAIN-NY-2B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (FEB-2001) to the EMBL; AF344235; AAK28956.1;
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                                                                                                    NCBI_TaxID=2234;
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5; Conserv
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5; Conservative
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1 (TrEMBLrel. 17,
1 (TrEMBLrel. 17,
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220 AA;
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24927 MW;
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                                                                                                                                                 Archaeoglobales;
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; Pred. No. 80;
4; Mismatches
    Tomb J.-F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
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Pred. No. 80;
4; Mismatches
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DNA polymerase gene encoded by
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DNA polymerase gene encoded
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    White
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                                                                                                                                                 Archaeoglobaceae,
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    Nelson
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RESULT
Q9F0L8
ID Q9F
AC Q9F
DT 01-
DT 01-
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C9OSK5
ID 09OSK5
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Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity

Matches 6; Conserv
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               OSFOL8 PRELIMINARY; PRT; 691 AA.

OSFOL6;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
GLUTAMATE SYNTHASE LARGE SUBUNIT (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O9QSK5 PRELIMINARY; PRT; 624 AA
O9QSK5;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence up
01-MAY-2000 (TrEMBLrel. 13, Last annotation
exoNUCLEASE II HOMOLOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

Muller K., Tidona C.A., Bahr U., Darai G.;

"The DNA sequence of Chilo iridescent virus
coordinates 0.974 and 0.101.";

Submitted (AUG-1998) to the EMBL/GenBank/DDB
EMBL; AF083915; AAD48147.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chilo iridescent virus
Viruses; dsDNA viruses,
NCBI_TaxID=10488;
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PfAm; PF00501; AMP-binding; 1.
PROSITE; PS00455; AMP_BINDING;
Hypothetical protein; Ligase; (
SEQUENCE 540 AA; 61888 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus."; nature 390,364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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2; Mismatche
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pred. No. 2.4e+02;
3; Mismatches (
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CGN GL
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Matches 5; Conservative
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01-OCT-2000 (TIEMBLIE1. 15, C
01-OCT-2000 (TIEMBLIE1. 15, I
01-OCT-2000 (TIEMBLIE1. 15, I
KIAA1403 PROTEIN (FRAGMENT).
KIAA1403.
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SEQUENCE
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BOYLE-VAVYA S., Ebert C.E., Daum R.S.;
BOYLE-VAVYA S., Ebert C.E., Daum R.S.;
Boyle-Vavya S., Ebert C.E., Daum R.S.;
The gltB gene encoding the large (a) subunit of glutamate synthase identified by screening a vancomycin-resistant Staphylococcus aureus library on medlum containing vancomycin.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF217184; AAG44102.1; -.
EMBL; AF217184; AAG44102.1; -.
                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat)
GLUTAMATE SYNTHASE LARGE SUBUNIT.
                                                                                             Q99WD1;
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TISSUE-BRAIN;
MEDLINE-20181126; PubMed-10718198;
MEDLINE-20181126; PubMed-10718198;
MEDLINE-20181126; PubMed-10718198;
Magase T., Kikuno R., Ishikawa K., Hirosawa M., Ohara O.;
Nagase T., Kikuno R., Ishikawa K., Hirosawa M., Ohara O.;
Prediction of the coding sequences of unidentified human genes
The complete sequences of 150 new cDNA clones from brain which
for large proteins in vitro.";
DNA Res. 7:65-73(2000).
EMBL; AB037824; BAA92641.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
NCBI_TaxID=1280;
[1]
Staphylococcus aureus Bacteria; Firmicutes;
                          GLTB OR SA0430.
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subsp. aureus N315.
Bacillus/Clostridium
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Last sequence update)
Last annotation update)
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Pred. No. 2.7e+02;
4; Mismatches 1;
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5.5e+02;
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Search completed: Job time: 285 sec

March 18,

2002, 09:51:56

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Best Local
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KUTODA M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.I., Nagai Y., Lian J., Ito T., Kanamori M.,
Matsunaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y.,
Takahashi N.K., Sawano T., Inoue R.I., Kaito C., Sekinizu K.,
Takahashi N.K., Sawano T., Inoue R.I., Kaito C., Sekinizu K.,
Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M.,
Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M.,
Ogasswara N., Hayashi H., Hiramatsu K.;
Ogasswara N., Hayashi H., Hiramatsu K.;
                                                                                                                                                "Whole genome sequencing of meticillin-resistant Staphylococcus aureus.";
Lancet 357:1225-1240(2001).
EMBL, AP003130; BAB41660.1;
Complete proteome.
Complete proteome.
1499 AA; 166259 MW; F20B82287BCF001C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus/Staphylococcus
NCBI_TaxID=158879;
 541
                               2 MAPEEIIMDR 11
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Pred. No. 6.
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29
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     AAY01812
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AAR11756
AAR12163
AAR12163
AAW26710
Peptide used to re
Human alpha-1-anti
Thrombin inhibitor
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Human PAI-1 P1-P1'
Human PAI-1 P2-P2'
Human PAI-1 P3-93'
Plasminogen activa
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  RESULT
ANYOLATE
ANY OBAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
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                                                                           Peptide composition
                                                                                                                                  WPI; 1999-288168/24
                                                                                                                                                                                                                                                                                         17-OCT-1997;
                                                                                                                                                                                                                                                                                                                                          15-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                              29-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9920295-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide used to regulate scuPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY01812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY01812 standard; peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3
                                                                                                                                                                                   Higazi AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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Human GTP-binding	AAB68542	22	163	89.7	26
S. cerevisiae cyto	AAB11409	21	N	89.7	26
Arabidopsis thalia	AAG55451	21	66	89.7	26
	AAG37027	21	N	93.1	27
	AAG46613	21	319	•	27
	AAB90794	22	0	00	29
Human Plasminogen	AAU04913	22	402	8	29
Human plasminogen	AAW31587	В	402	00.	29
Plasminoger	AAR07986 .	_	402	00.	29
Sequence of human	AAP81179		402	100.0	29
Beta plasminogen a	AAP82007		383	8	29
Modified mature Pl	AAR08411	_	382	8	29
Human Plasminogen	AAU04929	Ν	379	100.0	29
Human Plasminogen	AAU04928	22	379	00.	29
Human Plasminogen	AAU04927	22	379	00.	29
Human Plasminogen	AAU04926	22	379	8	29
Human Plasminogen	AAU04925	22	379	8	29
Human Plasminogen	AAU04924	22	379	8	29
_	$\sim$	22	379	100.0	29
_	AAU04922	22	379	8	29
Human Plasminogen	AAU04921	22	379	8	29
Human Plasminogen	AAU04920	22	379	8	29
Human Plasminogen	AAU04919	22	379	8	29
Human Plasminogen	AAU04918	22	379	8	29
Plasminogen activa	AAW26721	18	379	8	29
Plasminogen activa	AAW26720	18	379	•	29
Plasminogen activa	AAW26719	18	379	8	29
Plasminogen activa	AAW26718	18	379	8	29
_	AAW26717	18	379	8	29
_	AAW26716	18	379	8	29
_	AAW26715	18	379	8	29
act	AAW26714	18	379		29
	67	18	379	8	29
Plasminogen activa	AAW26712	18	379	100.0	29

## ALIGNMENTS

Example 1; Page 31; 63pp; English

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Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptides AAY01812-14 exemplify the peptide of the invention, which is used in a peptide composition to affect a biological process characterized by abnormal cell migration through a physiological barrier, to inhibit pai-1-dependent adhesion of a cell to a tissue, to promote clearance of scubA from the surface of a mammalian cell, and to impede pathological migration of a cell in a mammal. The composition can be used to affect a biological process characterized by abnormal cell migration through a physiological barrier, where the process is selected from anglogenesis, organogenesis, ovulation, inflammation, cancer, tumor cell invasion and metastasis, and atherosclerosis.
This sequence represents human alpha-1-antitrysin c-terminal peptide fragment 6. Alpha-1-antitrypsin is a known inhibitor of serine proteases, but loses its inhibitory activity due to a change in territary structure when cleaved by proteases such as leukocyte elastase. The cleaved alpha-1-antitrypsin molecules are cleared from the circulation through receptors in the liver and is accompanied by a depletion of extracellular cholesterol. The cause of this cholesterol depletion is due to an increase in the number of low density lipoprotein (LDL) receptors in liver cells which take up the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alpha-1-antitrypsin; fragment; low density lipoprotein; LDL; latherosclerosis; gallstone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human alpha-1-antitrypsin C-terminal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-DEC-1999
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                                                                                                                                                                                                                                                                                                                          (UYVI-) UNIV VIRGINIA COMMONWEALTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9945940-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY42738 standard;
                                                                                                                                                                       Disclosure; Page 5; 28pp;
                                                                                                                                                                                                       Lowering cholesterol levels in a patient using hypocholesterolemic peptide \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                              12-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                              10-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                16-SEP-1999
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1 eeiimd 6
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6; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                              99WO-US05139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Optionally N-terminally acetylated, tosylated,
myristoylated, benzoylated or carbobenzoxylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gment; cholesterol;
LDL; LDL receptor;
                                                                                                                                                                         English.
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Pred.
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4.3e+05;
thes 0;
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hypercholesterolaemia;
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RESULT
AAB92200
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       Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LDL cholesterol complex. This invention takes advantage of the fact that there is an increase in LDL receptor levels induced by the presence of cleaved alpha-1-antitrypsin and it derlyatives, including C-terminal peptide fragments. The C-terminal peptide fragments (AAY42733-Y42749) can be used to reduce the levels of LDL cholesterol in a patient and can be used to treat a wide variety of disorders, including atherosolerosis, hypercholesterolaemia and gallstones. As the peptides are derived from a naturally occurring human serum protein, they should not produce immune
The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various dispraces. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or
                                                                                                                                                                                                                                                                                                                                                                                                                   17-MAY-1999;
10-SEP-1999;
15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protection; endogenous therapeutic peptide; peptidase; cor
blood component; modification; succinimidyl; maleimido gro
hydroxyl; thiol; hormone; growth factor; neurotransmitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB92200 standard; Peptide; 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    side effects.
                                                                                                                                                                                                                    Disclosure; Page 646; 733pp; English.
                                                                                                                                                                                                                                                                    Modifying and attaching therapeutic peptides peptidase degradation, useful for increasing
                                                                                                                                                                                                                                                                                                                                                      Bridon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-MAY-2000; 2000WO-US13576.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thrombin inhibitor peptide SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-JUN-2001
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4 eeiimd
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                                                                                                                                                                                                                                                                                                                                                   DP, Ezrin AM,
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milarity 100.0%;
Conservative 0
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99US-0153406.
99US-0159783.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                      Holmes
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                                                                                                                                                                                                                                                                        to albumin prevents length of in vivo activity
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                                                                                                                                                                                                                                                                                                                                                          Thibaudeau K;
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05-MAR 1999
05-MAR 1999
09-MAR 1999
23-MAR 1999
25-MAR 1999
06-PR 1999
06-PR 1999
06-PR 1999
16-APR 1999
19-APR 1999
23-APR 1999
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23-APR 1999
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10-MAY 1999
06-MAY 1999
06-MAY 1999
11-MAY 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular uptake and interference with physiological processes. AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG32041 standard;
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Pred. No. 7.7;
0; Mismatches
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28. MAY. 1999
01. JUN. 1999
04. JUN. 1999
07. JUN. 1999
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Best Local Similarity 100.0%; 1
Matches 6; Conservative 0;
28-APR 1999
30-APR 1999
30-APR 1999
04-MAY 1999
05-MAY 1999
06-MAY 1999
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Pred. No. 49;
0; Mismatches
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AAR11756
ID AAR11756 standard; Protein; 379 AA.
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Matches 6
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Similarity 100.0%;
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99US-0149426
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99US-0162142
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                                                                                                                                                                               0
                                                                                                                                                                             Score 29; DB
Pred. No. 64;
0; Mismatches
                                                                                                                                                                               0
                                                                                                                                                                                                                 Length 284;
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence comprises mature PAI-1 in which Met(347) from the reactive centre (SCTVASSSTAVIVSARMAPERIMD) has been replaced by Ser from the corresponding site of ATII. The mutant PAI-1 is used to prevent reocclusion. It binds to vitronectin to act as a strong thrombin inhibitor, but is much less effective as a PA inhibitor. See also AARI1755 and AARI2162-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New plasminogen activator inhibitor 1 (PAI-1) mutants - comprise region of antithrombin III (ATIII), useful in fibrinolytic-thrombolytic therapy
          03-OCT-1989;
                                               03-OCT-1990;
                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                plasminogen activator inhibitor; antithrombin III; vitronectin; fibrinolysis; thrombolysis; serpin.
                                                                                                                                                                                                                                                          Human PAI-1 P2-P2'
                                                                                                                                                                                                                                                                                                   10-JUL-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                       AAR12162;
                                                                                                                                                                                                                                                                                                                                                                         AAR12162 standard; Protein; 379 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Page 24; 32pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pannekoek H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (STCL ) STICHT INST AND BLOEDTRAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plasminogen activator inhibitor; antithrombin III; vitronectin;
fibrinolysis; thrombolysis; serpin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human PAI-1 P1-P1' ATIII mutant.
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            89NL-0002454
                                               90WO-NL00145.
                                                                                                                                                                                                                                                            ATIII mutant.
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Pred. NO. 84;
0; Mismatches
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84;
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This sequence comprises mature PAI-1 in which residues 344-349 (1.e.SerAlaArgMetAlaPro) in the reactive centre has been replaced by AlaGlyArgSerLeuAsn from the corresponding site of ATII. The mutant PAI-1 is used to prevent reocclusion. It binds to vitronectin to act as a strong thrombin inhibitor, but is much less effective
                                                                                New plasminogen activator i region of antithrombin III thrombolytic therapy
                                                               Claim
                                                                                                                           WPI;
                                                                                                                                                                                         03-OCT-1989;
                                                                                                                                                                                                              03-OCT-1990;
                                                                                                                                                                                                                                                                                                                            Human PAI-1 P3-P3' ATIII mutant.
                                                                                                                                                                   (STCL ) STICHT
                                                                                                                                                                                                                                  18-APR-1991
                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                         plasminogen activator inhibitor;
                                                                                                                                                                                                                                                                                                                                                 10-JUL-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence comprises mature PAI-1 in which residues 345-348 (1.e.AlaArdWetAla) in the reactive centre has been replaced by GlyArgSerLeu from the corresponding site of ATIII. The mutant PAI-1s used to prevent reocclusion. It binds to vitronectin to act as strong thrombin inhibitor, but is much less effective as a PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New plasminogen activator inhibitor i (PAI-1) region of antithrombin III (ATIII), useful in thrombolytic therapy
                                                                                                                                                                                                                                                                                                                                                                                         AAR12163 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1991-132855/18
                                                                                                                                                                                                                                                                                              ibrinolysis;
                                                                                                                                                                                                                                                                                                                                                                                                      63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            also AAR11755-6 and AAR12163.
                                                                                                                           1991-132855/18
                                                               4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Page 24; 32pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                              thrombolysis; serpin.
                                                                                                                                                                    INST AND BLOEDTRAN
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                                                                                           ( inhibitor ( ATIII),
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Pred. No.
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Mismatches
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                                                                                                                                                                                                                                                                                                       antithrombin III; vitronectin;
                                                                                           1 (PAI-1)
useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12;
                                                                                           mutants - comprise fibrinolytic-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mutants - con
fibrinolytic-
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RESULT 1
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human plasminogen activator inhibitor (PAI-1) mature protein (see also AAW31587). It has an Ala for Arg substitution at amino acid cresidue 346, i.e. in the reactive centre loop of the protein. The mutant can be obtained by site-directed mutagenesis of PAI-1 DNA (see AAM797303) and expression in a host cell. Claimed PAI-1 mutants (see AAM797303) and expression in a host cell. Claimed PAI-1 mutants (see AAM797303) and expression in a host cell. Claimed PAI-1 mutants (see AAM797302) and expression in a host cell. Claimed PAI-1 mutants (see AAM797303) and sepecially at position 343 and/or 346, and may have additional stabilising mutantions comprising between one and four of His-50, Thr-154, Leu-319 and Ile-354, and one or more of Arg-333, Arg-335, Cly-331, Ile-372 and Leu-91. The mutants are characterised by being resistant to inactivation by elastase, plasminogen activator, plasmin, cathepsin G, chymase, gelatinases A and B, stromelysin and collagenase, and by having a high affinity tand the protection of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local
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See also
                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; Page -; 144pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasminogen activator-inhibitor type I mutant inhibits elastase - has high affinity for vitronectin, for therapeutic inhibition of elastase or vitronectin-mediated cell attachment, migration etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cystic fibrosis; atopic dermatitis; panoreatitis; restenosis; periodontal disease; arthritis; HIV; atherosclerosis; restenosis; neointima; fibrosis; wound healing; tumour; metastasis; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    plasminogen activator inhibitor type 1; pAI-1; human;
elastase; inhibitor; vitronectin; cell attachment; cell migration;
cell proliferation; emphysema; adult respiratory distress syndrome;
acute lung inflammation; alpha 1-antitrypsin deficiency;
                                                                                                                                                                                                                                                                                                                                                     This polypeptide comprises a preferred mutant, PlAla (R346A),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AMNA-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thrombosis;
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AAR11755-6
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Pred. No.
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RESULT 11
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Synthetic.
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                                                   Plasminogen activator-inhibitor type I mutant inhibits elastase has high affinity for vitronectin, for therapeutic inhibition of elastase or vitronectin-mediated cell attachment, migration etc.
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   Claim
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                                                                                                                                                                                                                                Stefansson
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Pred. No.
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Matches 6
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                                                                                                                                                                                     Homo sapiens.
Synthetic.
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                                                                                                                                                                                                                                                                                                       thrombosis; angiogenesis; therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               activator inhibitor mutant P1Gly (R346G).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC this polypeptide comprises a preferred mutant, PiGly (R346G), of Cd human plasminogen activator inhibitor (PAI-1) mature protein (see also AAW31587). It has a Gly for Arg substitution at amino acid CC residue 346, i.e. in the reactive centre loop of the protein. The CR mutant can be obtained by site-directed mutaqenesis of PAI-1 DNA CS (see AAP37303) and expression in a host cell. Claimed PAI-1 mutants CC (see AAW26710-25) have at least one amino acid substitution at position 343-350, especially at position 343 and/or 346, and may CC (see AAW26710-25) have at least one amino acid substitution at CC (see AAW26710-25) have at least one amino acid substitution at CC (see AAW26710-25) have at least one amino acid substitution at CC (see AAW26710-25) have at least one amino acid substitution at CC (see AAW26710-25) have at least one amino acid substitution at CC (see AAW26710-25) have at least one amino acid substitution at CC (see AAW26710-25) have at least one amino acid substitution at CC (see AAW26710-25) have at least one amino acid substitution at CC (see AAW26710-25) have at least one amino acid substitution between one and CC (see AAW26710-25) have at least to inactivation by elastase, CC (see AAW26710-25) have at least to collagenase, and by having a high affinity of vironase, gelatinases A CC (see AAW26710-25) have acid viry (specifically in emphysema, adult respiratory distress syndrome, acute lung inflammation, congenital CC panceratitis, periodontal disease, arthritis and HIV infection). They also inhibit vn-stimulated cell attachment, majoration and/or comparation involving pathological angiorential formation after vascular trauma, vascular graft restenosis, fibrosis (associated with CAPONIC inflammation or chemotherapy, or of the lung), wound condition involving pathological angiorential angiorents (aslociated with CAPONIC inflammation or chemotherapy, or of the lung), wound condition involving pathological angiorential angiorents and any condition involving pathological angiorential angiorents (as
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Best Local
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                  Plasminogen activator inhibitor
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350 eeiimd 355
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                                                                                                                                                                                                                                                                                                                               Conservative
                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       o acid sequence of the mutant protein was obtained the wild-type sequence provided in Fig 4A of the
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CC This polypeptide comprises a preferred mutant, Plasp (R346D), of CC human plasminogen activator inhibitor (PAI-1) mature protein (see also AAW31887). It has an Asp for Arg substitution at amino acid CC residue 346, i.e. in the reactive centre loop of the protein. The mutant can be obtained by site-directed mutagenesis of PAI-1 DNA CC (see AAW19730) and expression in a host cell. Claimed PAI-1 mutants (see AAW19730) and expression in a host cell. Claimed PAI-1 mutants (see AAW26710-25) have at least one amino acid substitution at comprising between one and CC four of His-150, Thr-154, Leu-319 and Ine-354, and one or more of CC characterised by being resistant to inactivation by elastase, and a stromelysin and collagenase, and by having a high affinity CC plasminogen activator, plasmin, cathepsin G, chymase, gelatinases A CC and B, stromelysin and collagenase, and by having a high affinity CC pathological elastase activity (specifically in emphysema, adult CC apha 1-antitrypsin deficiency, cystic fibrosis, atopic dermatitis, CC pancreatitis, periodonntal disease, restrictive and HIV infection), They also inhibit Vn-stimulated cell attachment, migration and/or Migration-induced proliferation (specifically in atherosclerosis, CC migration-induced proliferation (specifically in atherosclerosis, CC migration inflammation or chemotherapy, or of the lung), would the chronic inflammation or chemotherapy, or of the lung) would chaling with scarring and fibrosis, fibrosis (associated with CC trauma, vascular graft restenosis, floresis (associated with CC thronic inflammation or chemotherapy, or of the lung), would healing with scarring and fibrosis, growth/invasion of primary condition involving pathological angiogenesis (all claimed). Since the mutants are resistant to cleavage by the proteases to which they are more effective therapeutic agents. They also with path in the pathological angiogenesis (all claimed).
                                         by receptors.

(NB. the amino acid sequence of the mutant protein was obtained by adaptation of the wild-type sequence provided in Fig 4A of the specification).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasminogen activator-inhibitor type I mutant inhibits elastase - has high affinity for vitronectin, for therapeutic inhibition of elastase or vitronectin-mediated cell attachment, migration etc.
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Query Match Best Local S Matches 6

h 100.0%; Score 29; DB Similarity 100.0%; Pred. No. 84; 6; Conservative 0; Mismatches

DB 18; 84; es 0;

Length 379; Indels

0; Gaps

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CC This polypeptide comprises a preferred mutant, P4Ala (V343A), of CC human plasminogen activator inhibitor (PAI-1) mature protein (see CI also AAW31587). It has an Ala for Val substitution at amino acid CC residue 343, i.e. in the reactive centre loop of the protein. The mature amino acid commutant can be obtained by site-directed mutagenesis of PAI-1 DNA CC (see AAW26710-25) have at least one amino acid substitution at position 343-350, especially at position 343 and/or 346, and may CC have additional stabilising mutations comprising between one and CC four of His-150, Thr-154, Leu-319 and Ile-354, and one or more of CC Arg-333, Arg-333, Gly-331, Ile-372 and Leu-91. The mutants are CC plasminogen activator, plasmin, cathepsin G, chymase, gelatinases A CC and B, stromelysin and collagenase, and by having a high affinity CC for vitronectin (vn) and are used, in vivo or in vitro, to inhibit CC respiratory distress syndrome, actuel lung inflammation, congenital CC alpha 1-antitrypsin deficiency, cystic fibrosis, atopic dermatitis, periodontal disease, arthritis and HIV infection). They also inhibit Vn-stimulated cell attachment, migration and/or majoration-induced proliferation (specifically in atherosclerosis, CC trauma, vascular graft restenosis, fibrosis (associated with cc chronic inflammation or chemotherapy, or of the lung), wound cc healing with scarring and fibrosis, growth/invasion of primary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasminogen activator inhibitor type 1; PAI-1; human; elastase; inhibitor; vitronectin; cell attachment; cell migration; cell proliferation; emphysema; adult respiratory distress syndrome; acute lung inflammation; alpha 1-antitrypsin deficiency; acute fibrosis; atopic dermatitis; pancreatitis; periodontal disease; arthritis; HIV; atherosclerosis; restenosis; periodontal disease; arthritis; HIV; atherosclerosis; restenosis; neointima; fibrosis; wound healing; tumour; metastasis; psoriasis;
This polypeptide comprises a preferred mutant, P4Asp (V343D), of human plasminogen activator inhibitor (PAI-1) mature protein (see also AAW31587). It has an Asp for Val substitution at amino acid residue 343, i.e. in the reactive centre loop of the protein. The mutant can be obtained by site-directed mutagenesis of PAI-1 DNA (see AAW3973D3) and expression in a host cell. Claimed PAI-1 mutants (see AAW3973D3) and expression in a host cell. Claimed PAI-1 mutants position 343-350, especially at position 343 and/or 346, and may have additional stabilising mutations comprising between one and
                                                                                                                                                                                                                                                                                                                                                                       Plasminogen activator-inhibitor type I mutant inhibits elastase - has high affinity for vitronectin, for therapeutic inhibition of elastase or vitronectin-mediated cell attachment, migration etc.
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                                                                                                                                                                                                                                                                                                                 English.
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Pred. No. 84;
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is complex with PAI-1)
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CC Arg-333, Arg-335, Gly-331, Ile-372 and Leu-91. The mutants are CC characterised by being resistant to inactivation by elastase, CC plasminogen activator, plasmin, cathepsin G, chymase, gelatinases A CC and B, stromelysin and collagenase, and by having a high affility CC for vitronectin (Vn) and are used, in vivo or in vitro, to inhibit CP pathological elastase activaty (specifically in emphysema, adult respiratory distress syndrome, acute lung inflammation, congenital CC alpha 1-antitrypsin deficiency, cystic fibrosis, atopic dermatitis, particularly also inhibit Vn stimulated cell attachment, migration and/or migration-induced proliferation (specifically in atherosclerosis, congenital constrainty of the strainty vascular graft restenosis, neointime formation after vascular trauma, vascular graft restenosis, fibrosis (associated with Cc chronic inflammation or chemotherapy, or of the lung), wound changing with scarring and fibrosis, growth/invasion of primary condition involving pathological angiogenesis (all claimed). Since the budd, they are more effective therapeutic agents. They also promote uptake and clearance of elastase (or its complex with PAI-1) by receptors.

(NB. the amino acid sequence of the mutant protein was obtained by adeptation of the wild-type sequence provided in Fig 4A of the matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Best Local Smilarity 100.0%; Score 29; DB 18; Length 379; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps ob time: 365 sec
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Minimum DB
Maximum DB
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Perfect score:
Sequence:
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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3.575 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cgn2_6/ptodata/2/laa/5A_COMB.pep:*
/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
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US-08-781-020-6
US-09-038-93-6
US-08-840-204-3
US-08-8477-112-6
US-08-477-112-6
US-08-477-112-6
US-08-915-461-7
US-08-915-461-7
US-08-948-997-4
US-08-916-408-3
US-09-196-408-3
US-09-196-57-3
US-08-942-68-2
US-09-196-520-4
US-08-677-049-5
US-09-196-520-3
US-08-647-648-3
US-09-376-781-3
US-09-196-781-3
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Matches 6
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Result No.

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Sequence 8, Appl	۰20	8,	16		Sequence 2, App	Sequence 2, App	Sequence 4, Appl	Sequence 16, Appl	Sequence 8, App						•	Sequence 10, Ap

## ALIGNMENTS

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; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-781-020-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/08781020 Patent No. 5792749
                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Whitham, Michael E.
REGISTRATION UNMBER: 32,635
REFERENCE/DOCKET NUMBER: VCU-16
TELEPHONE: 703-391-2510
TELEPHAX: 703-391-9035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 20191

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/781,020

FILING DATE: 09-JAN 1997

CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                  TELEFAX: 703-391-9035
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wright, H. Tonie
TITLE OF INVENTION: METHOD AND COMPOSITION FOR LOWERING LOW
TITLE OF INVENTION: DEMSITY LIPOPROTEIN CHOLESTEROL
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: WHITHAM, CURTIS, WHITHAM & McGINN
STREET: Reston Intl. Center, 11800 Sunrise Valley Dr.,
STREET: Suite 900
CITY: Reston
STARE: '''
                                                                                                                                                                                                                                                              STRANDEDNESS:
1 EEIIMD 6
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                                                                                 h 100.0%; similarity 100.0%; of conservative 0;
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                                                                                                                                                                                                                                                                                                                                                          6:
                                                                                    Score 29; DB 1
Pred. No. 3.1;
0; Mismatches
                                                                                                                              DB 1; Length 33;
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-038-935-6
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Best Local Similarity 100.0%; Pred. No. 3.
Matches 6; Conservative 0; Mismatches
                                                         ATTORNEY/AGENT INFORMATION:
NAME: LIVNAY, SHMUEL
NAME: LIVNAY, SHMUEL
REGISTRATION UUMBER: 33,949
REFERENCE/DOCKET NUMBER: 30,80)
TELECOMMUNICATION INFORMATION:
TELEPHNE: (202) 897-1500
TELEFAX: (202) 822-016
TELEFAX: (202) 822-016
TELEFAX: 90-4030 MRSNFOERSWSH
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Janciauskiene, Sabina
APPLICANT: Janciauskiene, Sabina
TITLE OF INVENTION: LIPOPROTEIN CHOLESTEROL
FILE REFERENCE: 294022ba
CURRENT APPLICATION NUMBER: US/09/038,935
CURRENT FILING DATE: 1998-03-12
EARLIER APPLICATION NUMBER: 08/781,020
EARLIER FILING DATE: 1997-01-19
NUMBER OF SEQ ID NOS: 17
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                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
2IP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSER
STREET: 2000 PENNSYLVANIA AVENUE, NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPLICANT: LAWRENCE, DANIEL A.
PPLICANT: STEFANSSON, STEINGRIMUR P.
TILE OF INVENTION: MUTANT PLASMINOGEN ACTIVATOR-INHIBITOR
TILE OF INVENTION: TYPE 1 (PAI-1) AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EEIIMD 6
| | | | | | |
4 EEIIMD 9
                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE:
  STRANDEDNESS:
                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WASHINGTON
                     : 379 amino acids amino acid
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US-08-477-108A-6
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; TOPOLOGY: linear US-08-840-204-3
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US-08-121-714-6
                                                       Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION 1536
PRIOR APPLICATION UNMBER: 07/
FILING DATE: 09/01/92
APPLICATION NUMBER: 07/1
FILING DATE: 02/28/92
APPLICATION NUMBER: 07/6
FILING DATE: 07/67/
                                                                                                                                                                                                                   TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: WS-DOS (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER
                                                                                                                                                                                                                                         REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Sager,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  quence 6, Application US/08121714 tent No. 5470970
                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 390
                                                                                                                                                                                                                                                                                                                                   FILING DATE: 02/28/91
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADU...
STREET: ...
STREET: Massar
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373 EEIIMD 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ITLE OF INVENTION: MASPIN, A NOVEL SERPIN WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity es 6; Conserv
                1 EEIIMD 6
                                                                                                                                                           STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EEIIMD 6
                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Massachusetts
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                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ruth
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                                                                                                                                                                                                                                                                                             00530/072001
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Pred. No.
                                                                        Score 29; DB 1;
Pred. No. 37;
                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.0)
                                                                                     Length 390;
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                                                         Indels
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                                                         Gaps
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Sequence 6, Application US/08477112 Patent No. 5905023
                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Sager, Ruth
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                                                                                                                                                 TITLE OF INVENTION: MASPIN, TITLE OF INVENTION: TUMOR SINUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 390
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                     373 EEIIMD 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 02/28/91
ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM: MS-DOS (Version 5 SOFTMARE: Wordberfeet (Version 5.1) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/477,108A FILING DATE: June 7, 1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" DI
                                                                                                                         RRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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TOPOLOGY: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EEIIMD 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 0
FILING DATE: 09/01/92
APPLICATION NUMBER: 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ITLE OF INVENTION: MASDIN, A NOVEL SERVIN WITH
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                                                        Boston
                                                              225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Massachusetts
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5801001
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                                                                                      Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fish & Richardson P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Franklin Street
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                                                                                                                                                            N, A NOVEL SERPIN WITH SUPPRESSING ACTIVITY
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Best Local Similarity 100.0
***Tches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application PC/TUS9308322
GENERAL INFORMATION:
APPLICANT: Sager, Ruth
TITLE OF INVENTION: MASPIN, A NOV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
LENGTH: 390
TYPF:
CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/
APPLICATION O9/01/92
                                                                                                                                                    SOFTWARE: WORDPERIECT CURRENT APPLICATION DATA:
                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
                                                                                                                                                                                                                                                                              COUNTRY: U.S.
COUNTRY: U.S.
02110-2804
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373 EEIIMD 378
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PRIOR APPLICATION DATA.
APPLICATION UMBER: 08
FILING DATE: 09/01/93
APPLICATION UMBER: 09/01/92
FILING DATE: 09/01/92
                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER
APPLIC
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MEDIUM TYPE: 3.5" Diskette,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Fraser, Janis
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
SOFTWARE: WordPer
                                                                                                                                                                                                                                                                                                                                                                                  Boston
                                                                                                                                                                                                                                                                                                                            Massachusetts: U.S.A.
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Y: U.S.A.
                                                                                                                                                                       WordPerfect (Version 5.1)
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SYSTEM: MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MASPIN, A NOVEL SERPIN WITH TUMOR SUPPRESSING ACTIVITY
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                                                                                                                         PCT/US93/08322
                                07/938,823
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               502 or 555X
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Gaps

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TELEFAX:

JS-08-477-112-6

DRESSEE:

Query Match Best Local : Matches

6;

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Matches
          REFERENCE/POCKET NUMBER: UMIC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEPAX: (512) 474-7570
NFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match .
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                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/315,461
FILING DATE: Concurrently Herewith
CLASSIFICATION: 530
                                                                                                                                                  NAME: PACKET INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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NFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                       COUNTRY: CT. 77210
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5970
TELEFAX: (617) 542-8906
                                                                                                                   NAME: Parker, David L. REGISTRATION NUMBER: 32,165
                                                                                                                                                                                                                                                                                                                                                          CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Arnold, Wh
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                       ER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPLICATION NUMBER:
ILING DATE: 02/28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7, Application US/08315461
. 5639726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shore,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lawrence, Daniel A.
Sinsburg, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Steven T
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                                                                                                       UMIC:006
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 5; Length 390;
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                         US-08-840-204-2
Sequence 2, Application US/08840204
Patent No. 6103498
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                                                                                      373 EEIIMD 378
                                                                                                            1 EEIIMD 6
                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                          CENGTH:
                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
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; MOLECULE TYPE: protein US-08-948-997-4
     Query Match 100.0%; Score 29; DB 3; Length 402; Best Local Similarity 100.0%; Pred. No. 38; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk.
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/948,997
FILING DATE: Oct-10-97
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: A. ANDERS BROOKES
REGISTRATION NUMBER: 35,373
REGISTRATION NUMBER: 35,373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single;
TOPOLOGY: linear;
MOLECULE TYPE: protein
US-08-315-461-7
                                                                                                                                                                                                                           TELEFAX: (301) 309-85
INFORMATION FOR SEQ ID NO:
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Best Local Similarity 100.0%;
Matches 6; Conservative (
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                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: HASTINGS, GREGG
APPLICANT: COLEMAN, TIM
APPLICANT: LAWRENCE, DANIEI
                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    373 EEIIMD 378
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TISSUE-TYPE PLASMINOGEN ACTIVATOR
                                                                                                                                                                                                                                                                                            PF336
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Pred. No.
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 Gaps
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; TYPE: PRT
; ORGANISM: BOS
US-09-348-817A-4
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Query Match
Best Local Similarity
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Best Local Similarity 100.0%;
Matches 6; Conservative 0
                                                                                                                                    SEQ ID NO 4
                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/348,817A
CURRENT FILING DATE: 1999-07-08
PRIOR APPLICATION UNMBER: 08/948,997
PRIOR FILING DATE: 1997-10-10
PRIOR APPLICATION NUMBER: 60/028,117
PRIOR FILING DATE: 1996-10-11
                                                                                                                                                                                                                                                                                                                                                                                             09-348-817A-4
                                                                                                                                                                                                                                                                                                                                                            equence 4, Application US/09348817A
atent No. 6191260
                                                                                                                                                                 MBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                              TLE OF INVENTION: Brain-Associated Inhibitor of Tissue-Type Plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (202) 822-0168
TELEX: 90-4030 MRSNFOERSWSH
NFORMATION FOR SEQ ID NO: 2:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: LIVNAT, SHMUEL
REGISTRATION NUMBER: 33,949
REFERENCE/DOCKET NUMBER: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                            INFORMATION:
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2000 PENNSYLVANIA AVENUE, NW
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100.0%;
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Score 29;
Pred. No.
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38;
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                                                                   NERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
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APPLICATION NUMBER: US 60/024,056
FILING DATE: 16-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COPTRADED: DECEMBER PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/934,011
FILING DATE: 15-AUG-1997
                                                                                                                                                                                              1 EEIIMD 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTLE OF INVENTION: PANCREAS-DERIVED PLASMINOGEN ACTIVATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                               ECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  ELEPHONE:
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                                                                                9, Application US/08796899
6160202
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6; Conserv
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APPLICATION DATA:
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                                BUSTOS, Mauricio M
CHERN, Maw-Shenq
                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                           es: single
linear
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MODIFICATION OF SEED CROPS WITH TRANSCRIPTION FACTORS
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                                                                                                                                                                                                                                     Score 29;
Pred. No.
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                                                                                                                                                                                                                                                 DB 4;
                                                                                                                                                                                                                                                 Length 402;
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COUNTRY:

DDRESSEE:

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STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
US-08-796-899-29
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Best Local Similarity
Matches 5; Conserv
                                                                            COMPUTER: HP VECTEA 486/33
OPERATING SYSTEM: MSDOS VER:
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/96
FILING DATE:
                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (703) 836-20 NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                       ORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        380 EEIILD 385
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APPLICATION NUMBER: US 08/319,544
FILING DATE: 07-CCT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COMMUNENT: PTTTM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                    INFORMATION:
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22313-1404
                                                                                                                                                                                                                                                        E: Human Genome Sciences, Inc. 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                           Application US/08961083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3: Burns, Doane, Swecker & Mathis P.O. Box 1404
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06-FEB-1997
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) 836-2021

NO: 29:
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                                                                                           US/08/961,083
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 26; |
Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 551;
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                                                                                US-09-019-942-3
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Best Local Similarity
Watches 4; Conserve
                                                                                                                                                              TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                          FILING DATE:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anit
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 0733
TELECOMMUNICATION INFORMATION:
TELEPHONE: 61/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -09-019-942-3
Sequence 3, Application US/09019942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 6033855
GENERAL INFORMATION:
                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/019,942
FILING DATE: 06-FEB-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Ri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NFORMATION FOR SEQ ID NO:
                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: MA
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                                                                                                                                       CENGTH:
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hypothetical protein grpE [imported] - Escherichia coli (strain 0157:H7) C;Species: Escherichia coli (c;Species: Escherichia coli (c;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001 C;Accession: H85907 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, Nature 409, 529-533, 2001 A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7. A;Reference number: A85480; MUID:21074935; PMID:11206551
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A; Residues: 1-197 < LIP
A; Cross-references: EMBL: X07863; NID: 941618; PIDN: CAA30711.1;
A; Cross-references: EMBL: X07863; NID: 941618; PIDN: CAA30711.1;
A; Blattner, F. R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.;
A; Rose, D.J.; Mau, B; Shao, Y
Science 277, 1453-1462, 1997
Science 277, 1453-1462, 1997
A; Title: The complete genome Sequence of Escherichia coli K-12
A; Reference number: A64720; MUID: 97426617
A; Accession: A65040; MUID: 97426617
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                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: grpE
C;Superfamily: heat shock protein grpE
F;2-197/Product: heat shock protein B25.3 #status
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wis, D., Nierman, W.C., .....
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA, A;Residues: 1-197 <5T0>
A;Residues: 1-197 <5T0>
A;Cross-references: GB.AE005174; NID:g12517038; PIDN:AAG57724.1; GSPDB:GN00145; A;Experimental source: strain 0157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                               R;Chuang, T.H.; Hamilton, R.T.; Nilsen-Hamilton, M. Gene 162, 303-308, 1995
A;Title: Cloning of the mink plasminogen activator A;Reference number: JC4265; MUID:96032362
A;Accession: JC4265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plasminogen activator inhibitor type 1 precursor - C;Species: Mustela vison (American mink) C;Date: 19-0ct-1995 #sequence_revision 08-Feb-1996 C;Accession: JC4265
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C;Superfamily: heat shock protein grpE
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A; Residues: 1-400 <CHU>
A; Cross-references: EMBL: X58541; NID: g1164923; PID:
A; Experimental source: lung CCLG4 epithelial cells
C; Comment: This protein controls the activities of
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A; Residues: 1-284 <STO>
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.; Koo, H.; Moffat,
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;Superfamily: antithrombin III
;Keywords: glycoprotein; plasminogen activator; serine proteinase inhibitor;
;1-21/Domain: signal sequence *status predicted <SIG>
;22-400/Product: plasminogen activator inhibitor type 1 *status predicted <
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Tallon, L.
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A; Molecule type: DNA
A; Residues: 85-86;88-93;166-171;231-236;298-302;331-336;360-365;388-393 <FOL>
A; Residues: 85-86;88-93;136; NID:q189543
A; Cross Treferences: GB:M33136; NID:q189543
A; Note: sequences of the intron/exon boundaries are shown
A; Note: sequences of the intron/exon boundaries are shown
A; Namekoek, H.; Veerman, H.; Lambers, H.; Diergaarde, P.; Verweij, C.L.; van
EMBO J. 5, 2539-2544, 1986
BMBO J. 5, 2539-2544, 1986
A; Title: Endothelial plasminogen activator inhibitor (PAI): a new member of t
A; Reference number: A91052; MUID:87053819
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C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 08-Dec-2000
C;Accession: A28107; S02551; A26996; I59126; JS0397; A25693; A26146; A29100;
C;Accession: A28107; S02551; A26996; I59126; JS0397; A25693; A26146; A29100;
C;Bosma, P.J.; van den Berg, E.A.; Koolstra, T.; Siemieniak, D.R.; Slightom,
J. Biol. Chem. 263, 9129-9141, 1988
A;Title: Human plasminogen activator inhibitor-1 gene. Promoter and structura
A;Reference number: A28107; MUID:88243790
A;Accession: A28107; MUID:88243790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:J03836; NID:g189579; PII
R;Follo, M.; Ginsburg, D.
Gene 84, 447-453, 1989
A;Title: Structure and expression of the human
A;Reference number: JS0397; MUID:90128289
A;Accession: JS0397
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A; Residues: 1-14. 'T', 16-402 <STR>
A; Residues: 1-14. 'T', 16-402 <STR>
A; Residues: 1-14 by the complete translation is not annotated in GenBank entries Hspall1, Hspall2
A; Note: the complete translation is not annotated in GenBank entries Hspall1, Hspall2
R; Loskutoff, D.J; Linders, M.; Keljer, J.; Veerman, H.; van Heerlkhulzen, H.; Pannek
Biochemistry 26, 3763-3768, 1987
Biochemistry 26, 3763-3768, 1987
A; Title: Structure of the human plasminogen activator inhibitor 1 gene: nonrandom dis
A; Reference number: A26996; MUID: 88000586.
A; Accession: A36996
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A;Molecule type: LONA
A;Residues: 1-402 <LOS>
A;Residues: 1-402 <LOS>
A;Residues: 1-408
A;Cross·references: GB:M22321; GB:M17121; NID:g189576; PIDN:AAA60009.1; PID:g189578
A;Cross·references: GB:M22321; GB:M17121; NID:g189576; PIDN:AAA60009.1; PID:g189578
A;Note: the sequence in GenBank entry HUMPAIE2; release 109.0, (PID:g189578) has the
A;Note: the sequence in GenBank entry HUMPAIE2; release 109.0, (PID:g189578) has the
B;Note: the sequence in GenBank entry HUMPAIE2; release 109.0, (PID:g189578) has the
B;Note: the sequence in GenBank entry HUMPAIE2; release 109.0, (PID:g189578) has the
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B;Note: the sequence in GenBank entry HUMPAIE2; release 109.0, (PID:g189578) has the
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B;Note: the sequence in GenBank entry HUMPAIE2; release 109.0, (PID:g189578) has the
B;Note: the sequence in GenBank entry HUMPAIE2; release 109.0, (PID:g189578) has the
B;Note: the sequence in GenBank entry HUMPAIE2; release 109.0, (PID:g189578) has the
B;Note: the sequence in GenBank entry HUMPAIE2; release 109.0, (PID:g
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N;Alternate names: plasminogen activator inhibitor, endothelial
                                                                                                        A; Residues: 1-402 < PAN>
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A; Residues: 1-9 <20N>
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A;Reference number: I59126; MUID:88289754
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Strandberg, L.; Lawrence, D.; Ny, T.
ur. J. Biochem. 176, 609-616, 1988
;Tittle: The organization of the human-plasminogen-activator-inhibitor-1 gene. Implic;Reference number: S02551; MUID:89005111
;Accession: S02551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;230,286,350/Binding site: carbohydrate (Asn) (covalent) #status predicted;367/Inhibitory site: Arg (plasminogen activator) #status predicted
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ces: GB:X04429; NID:g35271; PIDN:CAA28025.1; PID:g35272
2eheb, R.; Yang, A.Y.; Rafferty, U.M.; Andreasen, P.A.;
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J.L.
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Nielsen,

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A; Molecule type: protein
A; Residues: 370-375 <370
C; Comment: This inhibitor acts as "bait" for tissue plasminogen activator (see PIR:UKHUT)
C; Comment: This inhibitor acts as "bait" for tissue plasminogen activator (see PIR:UKHUT)
C; Comment: Three types of PAI have been identified (see also PIR:A32853 and PIR:A39339);
oma cells. Vascular endothelial cells may be the primary site of synthesis of plasma PAI
C; Comment: Glycosylation is not required for inhibitory activity.
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A; Residues: 364-402 < AND2>
A; Residues: 364-402 < AND2>
A; Cross-references: GB: X04731; NID: g35260; PIDN: CAA28442.1; PID: g35261
A; Cross-references: GB: X04731; NID: g35260; PIDN: CAA28442.1; PID: g35261
A; Cross-reference constance: GB: X04731; NID: g35260; PIDN: CAA28442.1; PID: g35261
A; Title: Isolation of multiple types of plasminogen activator inhibitors from vascular A; Reference number: A60436; MUID: g0020174
A; Accession: A60436
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A; Residues: 17-402 < WUN>
A; Residues: 17-402 < WUN>
A; Residues: 17-402 < WUN>
A; Cross-references: GB: X04744; NID: g35275; PIDN: CAA28444.1; PID: g755747
A; Cross-references: GB: X04744; NID: g35275; PIDN: CAA28444.1; PID: g755747
A; Note: part of this sequence, including the amino end of the mature protein, was confix R; NY, T.; Sawdey, M.; Lawrence, D.; Millan, J.L.; Loskutoff, D.J.
R; NY, T.; Sawdey, M.; Lawrence, D.; Millan, J.L.; Loskutoff, D.J.
Proc. Natl. Acad. Sci. U.S. A. 83, 6776-6780, 1986
A; Title: Cloning and sequence of a cDNA coding for the human beta-migrating endothelial-
A; Reference number: A25895; MUID: 86313660
C;Superfamily: antithrombin III
C;Roywords: glycoprotein; serine proteinase inhibitor
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-402/Product: plasminogen activator inhibitor-1 #status experimental
F;232,288,352/Binding site: carbohydrate (Asn) (covalent) #status predict
                                                                                                                                                        A;Gene: GDB:PAI1; PLANH1
A;Cross references: GDB:120297; OMIM:173360
A;Map position: 7921.3-7922
A;Introns: 91/1; 169/1; 234/1; 300/2; 334/1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Stroemqvist, M.; Karlsson, K.E.; Bjoerquist, P.; Andersson, Biochim. Blophys. Acta 1295, 103-109, 1996
A;Title: Characterization of the complex of plasminogen activa A;Reference number: S70346; MUID:96283799
A;Accession: S70346
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Kjoller, L.; Martensen, P.M.; Sottrup-Jensen, L.; Justesen Eur. J. Blochem. 241, 38-46, 1996
A;Title: Conformational changes of the reactive-centre loop A;Reference number: S74133; MUID:97054589
A;Accession: S74133
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A; Residues: 225-235 <LAU>
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A; Title: cDNA cloning of human plasminogen activator-inhibitor from endothelial cells.
A; Reference number: A92766; MUID:87058123
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A; Residues: 22-30; 370-376 < KJO>
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A; Residues: 1-14,'T', 1
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A; Residues: 20-402 < NYT>
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ett. 210, 11-16, 1987
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A;Molecule type: mRNA
A;Residues: 153-235 <PEP>
A;Cross-references: EMBL:X52906; NID:g598; PIDN:CAA37094.1; PID:g930005
A;Title: Bovine endothelial cell plasminogen activator inhibitor. Purification and he A;Title: Bovine number: S01324; MUID:g59972
A;Accession: S01324
A;Access
hypothetical protein BB0205 - Lyme disease spirochete
(C;Species: Borrelia burgdorferi (Lyme disease spirochete)
(C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 28-Jul-2000
(;Accession: E70125
R;Fraser, C.M.; Cdsjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, I
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, I
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hat
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N;Alternate names: endothelial-cell plasminogen activator inhibitor; PAI-1
C;Specles: Bos primigenius taurus (cattle)
C;Date: 28-Feb-1990 #sequence_revision 22-Apr-1995 #text_change 18-Jun-1999
C;Accession: $06745; A53855; $01324; $10906
R;Mimuro, J.; Sawdey, M.; Hattori, M.; Luskutoff, D.J.
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A; Residues: 1-402 - WIM>
A; Cross-references: EMBL:X16383; NID:9600; PIDN:CAA34419.1; P
A; Cross-references: EMBL:X16383; P
A; Cross-references: EMBL:X16383; P
A; Cross-references: EMBL:X16383; P
A; Cross-references: EMBL:X16383; P
A; Cross-references: EMBL:
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Nucleic Acids Res. 17, 8872, 1909
A;Title: cDNA for bovine type 1 plasminogen activator
A;Reference number: S06745; MUID:90067867
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cids Res. 17, 8872, 1989
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A35855; MUID:90338128
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Pred. No.
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A;Map position: 2
A;Introns: 22/1; 61/3; 372/2; 474/1
C;Superfamily: Caenorhabditis elegans hypothetical protein Y51HlA.6
                                                                                                                             A; MoLecule type: DNA
A; Residues: 1-574 <WIL>
A; Cross-references: EMBL: ALO32644;
A; Experimental source: clone Y51HlA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Map position: 12R
C; Superfamily: nodB homology
F; 113-264/Domain: nodB homology
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A:Reference number: S51437
A:Accession: S51439
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C;Date: 23-Feb-1995 #sequence_revision 12-May-1995 #text_change 05-Nov-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genemic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943
A;Accession: E70125
                                                                                                                                                                                                          A;Accession: T27100
A;Status: preliminary; translated from
                                                                                                                                                                                                                                         submitted to the EMBL Data Library, October 1998 A;Reference number: Z20309 A;Recession: T27100
                                                                                                                                                                                                                                                                                                                                            hypothetical protein Y51H1A.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct_1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Pauley, A.
submitted to the EMBL Data Library, November 1994
submitted to the EMBL Data Library, November 1994
submitted to the EMBL Data Library, November 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein YLR307w - yeast (Saccharomyces N;Alternate names: hypothetical protein L2142.2
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A; Residues: 1-525 < KLE>
                                                                                    A; Gene: CESP:Y51H1A.6
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                                                                                                            Genetics:
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Pred. No.
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67;
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                   polyhedrin - Galleria mellonella nuclear polyhedrosis virus (tentative seque N;Alternate names: inclusion body protein C;Species: Galleria mellonella nuclear polyhedrosis virus C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 31-Mar-2000 C;Accession: JN0407
R;Gusak, N.M.; Kozlov, E.A.; Ovander, M.N.; Serebryany, S.B.
Bioorg, Khim. 7, 996-1007, 1981
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A; Residues: 1-120 <DEA>
A; Cross-references: EMB
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A;Description: electron transfer C;Superfamily: cytochrome b5; cytochrome b5 core homology C;Superfamily: cytochrome b5; cytochrome b5 core homology c;Reywords: electron transfer; heme; iron; metalloprotein; transmembrane protein F;2-77/Domain: cytochrome b5 core homology <CB5> F;102-118/Domain: transmembrane #status predicted <TMM> F;37,61/Binding site: heme iron (His) (axial ligands) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-16, (0', 18-120 <TRU>
A;Residues: 1-16, (0', 18-120 <TRU>
A;Cross-references: EMBL:L22499; NID:9431761; PIDN:AAA67468.1; PID:9431762
A;Cross-references: EMBL:L22499; NID:96 Sartorello, F.; Pandolfo, D.; Lanfranchi,
Bubmitted to the EMBL Data Library, February 1996
A;Description: The DNA sequence of cosmid 14-13b from chromosome XIV of Saccharomyces
A;Reference number: S67327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Reference number: 563047
A;Recession: S63052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Truan, G.; Epinat, J.C.; Rougeulle, C.; Cullin, C.; Pompon, D. Gene 149, 123-127, 1994
A;Title: Cloning and characterization of a yeast cytochrome b(5)-encoding A;Reference number: $47919; MUID:95047457
A;Accession: $47919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:271387; NID:g1302031; PIDN:CAA95990.1; PID:g1302032; MIPS:YN A;Experimental source: strain S288C R;Truan, G.; Epinat, J.C.; Rougeulle, C.; Cullin, C.; Pompon, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytochrome b5 - yeast (Saccharomyce N;Alternate names: protein N1949; p C;Species: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: SGD:S0005055; MIPS:YNL111c
                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-120 <-DAN>
A;Cross-references: EMBL:269382; NID:gl183941; PIDN:CAA93396.1; PID:gl183962
Similarity 83.5
5; Conservative
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es: protein N1949; protein YNL111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 27; DB
Pred. No. 1.4e
2; Mismatches
                                 Score 26; DB 2;
Pred. No. 41;
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         Mismatches
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se, April 1996
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1.4e+02;
         0
                                                             Length 120
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sequence) (fra

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A;Title: Tryptic peptides of inclusion body protein of nu A;Reference number: JN0407
A;Recession: JN0407
A;Molecule type: protein A;Residues: 1-240 <GUSS
A;Note: 18-Arg. 7-Ala, 87-Gly, 126-Met and 139-Glu were C;Superfamily: nuclear polyhedrosis virus polyhedrin C;Keywords: polyhedrin
                                                                                                            A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-274 «KAW>
A;Cross-references: GB:AJ248284; GB:AL096836; NID:g5457730; PIDN:CAB49533.1; PID:g545804
A;Experimental source: strain Orsay
                                                                                                                                                                                                      R: anonymous, Genoscope
Submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome
A;Reference number: A75001
A;Accession: F75181
                                                                                                                                                                                                                                                                                                                                                                                                                                                     무
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-274 < KAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguch DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic A;Reference number: A71000; MUID:98344137
A;Accession: D71032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable autoantigen like protein - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000
C;Accession: D71032
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A;Experimental source: strain OT3
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                                                                                                                                                                                                                                                                                              ;Species: Pyrococcus abyssi
;Date: 20-Aug-1999 #sequence_revision
;Accession: F75181
                                                        Superfamily: conserved
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Best Local Similarity
Matches 4; Conserv
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Pred. No.
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Pred. No. le+02;
2; Mismatches
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213 EELVMD
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C;Genetics:
A;Gene: aq_814
C;Superfamily: Aeropyrum pernix hypothetical protein APE2212
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                                                                                                                                                                                                                                                                                                                                                                                             A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A;Reference number: A70300; MUID:98196666 A;Accession: A70371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         conserved hypothetical protein aq_814 - Aquifex aeolicus C;Species: Aquifex aeolicus C;Species: Aquifex aeolicus C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 20-Jun-2000 C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 20-Jun-2000 C;Accession: A70371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-284 <ARN>
A;Residues: 1-284 <ARN>
A;Cross-references: GB:AE001755; GB:AE000512; NID:g4981432; PIDN:AAD35997.1; PID:g498
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM0916
C;Superfamily: Aeropyrum pernix hypothetical protein APE2212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 399, 323-329, 1999
A,Title: Evidence for lateral gene transfer between
A;Reference number: A72200; MUID:99287316
A;Accession: C72320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  conserved hypothetical protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: C72320
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft,
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Ri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 392, 353-358, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Deckert, G.; Warren, P.V.; Gaasterland,
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Best Local Similarity
Matches 5; Conserv
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Matches 4; Conservative
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5; Conservative
147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 1.1e
1; Mismatches
                                                                                      Score 26; DB 2;
Pred. No. 1.1e+02;
1; Mismatches
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2; Mismatches
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Maximum DB seq length: 2000000000
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Perfect score:
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       Query
Match
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Gapop 10.0 , Gapext 0.5
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29
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Copyright (c) 1993 - 2000 Compugen Ltd.
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GRPE_BCÓLI
PAII_MUSVI
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CDA2_YEAST
CYBS_YEAST
RPB6_ASEPI
Y199_CABEIN
Y199_CABEIN
Y199_CABEIN
Y199_CABEIN
CLPX_LACLA
LIPA_DEIRA
CLPX_LACLA
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CLPX_LACLA
Y878_METJA
HELI_HSV7J
SLPM_BACST
XSPM_SUSSE
USBE_STREA
CSPA_MOUSE
USBE_STREA
RES_TREA
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4 african swi
6 methanococc
4 haemophilus
2 caenorhabdi
1 methanococc
7 escherichia
1 clostridium
9 african swi
8 cenorhabdi
8 cenorhabdi
6 deinococcus
6 hactococcus
6 hactococcus
6 hactococcus
7 escherichia beri
8 methanococc
7 human herpe
7 human herpe
7 human herpe
7 human herpe
8 hacillus po
1 thermoplasm
9 saccharomyc
8 bacillus sp
1 saccharomyc
8 pacillus sp
1 staphylococ
7 escherichia
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shi H uchi T. uchi	OM N.A.?  MG1655;  MG1655;  R., Plunkett G. I R., Plunkett G. I Davis N.W., Kirkp; O Y.; O Y.; O Y.; OM N.A.  14980; PubMed-920 A 191ba H., Baba T mura S., Kitagawa n., Mori H., Nakad	10, Creation Creation Coreation Coff Coff Coff Coff Coff Coff Coff Co	STANDARD;
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ada C hia c p and p and timul	nd V., F., hi N.,	(HSP24). laceae;	thermotoga  homo sapien  klebsiella  mus musculu  mus musculu  raynechocyst  raynechocyst  raynerichia  raynerichia  daquifex aeo  caenorhapilus  thermoplasm  homo sapien  homo sapien

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P50449;
DT 01-OCT-1996 (Rel. 34, Created)
DT 02-AUG-2001 (Rel. 34, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PLASMINGEN ACTIVATOR INHIBITOR: 1 PRECURSOR (PA
DE PLASMINGEN ACTIVATOR INHIBITOR) (PAI).

**RPINE1 OR PAII OR PLANH1 OR PAI-1.

**RPINE1 OR PAII OR PLANH1 OR PAI-1.

**Chordata; Craniata; Verte
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Best Local
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SWISS-2DPAGE; P09372; COLI.

ECOZDBASE; B075.3; 6TH EDITION.

ECOGENE; EG10416; 97pE.

InterPro; IPR000740; GrpE; 1.

Pfam; PF01025; GrpE; 1.

PRINTS; PR00773; GRPEPROTEIN.

PRONTS; PS01071; GRPEPROTEIN.

PROSITE; PS01071; GRPE; 1.

Chapperone; Heat shock; 3D-structure; Complete proteome.

Chapperone; Heat shock; 3D-structure; Complete CRC64;
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-97258949; PubMed-9103205;
Harrison C.J., Hayer-Hartl M., di Liberto M., i Harrison C.J., Hayer-Hartl M., di Liberto M., i Harrison C.J., Hayer-Hartl M., di Liberto M., i Harrison C.J., Harrison C.J., Harrison C.J., JOINTLY WITH DNAJ, TO DNAK, HELPS TO RELEASE ADP FROM DNAK THUS
MEDLINE=96032362: PubMed=7557448:
Chuang T.H., Hamilton R.T., Nilsen-Hamilton
"Choning of the mink plasminogen activator 1
RNA: an mRNA with a short half life.";
RNA: an flow 1905)
-1- FUNCTION: THIS INHIBITOR ACTS AS "BAIT"
ACTIVATOR, UROKINASE, AND PROTEIN C. ITS
                                                                                                            Mustela vison (American mink).
Eukaryota; Metazoa; Chordata; Craniata; Ven
Mammalla; Eutheria; Carnivora; Fissipedia;
CCBI_TaxID-9667;
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INDUCTION: BY THE SIGNA(32) SUBUNIT OF INICATITY: BELONGS TO THE GRPE FAMILY.
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ia; Mustelidae; Mustela.
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ITS RAPID INTERACTION WITH
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                                            n M.;
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e factor GrpE bound
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p13909;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last seque
20-AUG-2001 (Rel. 40, Last annot
PLASMINOGEN ACTIVATOR INHIBITOR-
PLASMINOGEN ACTIVATOR INHIBITOR
PLASMINOGEN ACTIVATOR INHIBITOR
SERPINEL OR PAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus (Bovine).
Eukaryota; Metazoa; Cl
Mammalia; Eutheria; Co
Bovidae; Bovinae; Bos
NCBI_TaxID-9913;
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Pfam; PF00079; serpin; 1.
SMART; SM00093; SERPIN; 1.
PROSITE; PS00284; SERPIN; 1.
Serpin; Serine protease inhibitor;
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TISSUE-Adrenal cortex;
MEDLINE-90338128; PubMed-1696269;
MEDLINE-90338128; PubMed-1696269;
Pepper M.S., Belin D., Montesano R., Orci L., Vassalli J.-D.;
*Transforming growth factor-beta 1 modulates basic fibroblast growth factor-induced proteolytic and angiogenic properties of endothelial
                                                                                                                                                                                                                                                             Katagiri K., Okada K., Hattori H., Ye
"Bovine endothelial cell plasminogen
Purification and heat activation.";
Eur. J. Biochem. 176:81-87(1988).
                                                                                                                                                                                                                                                                                                                                                                     | (2) | (2) | (2) | (3) | (4) | (4) | (5) | (5) | (6) | (6) | (6) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) | (7) 
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MEDLINE-90067867; PubMed-2587231;
Mimuro J., Sawdey M., Hatiori M., Loskutoff D.J.;
*CDNA for bovine type 1 plasminogen activator inhibitor (PAI-1).*;
Nucleic Acids Res. 17:8872-8872(1989).
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activator
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(GLCNAC. .) (POTENTIAL)
(GLCNAC. .) (POTENTIAL)
(GLCNAC. .) (POTENTIAL)
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Best Loc
Matches
SEQUENCE FROM N.A.

MEDLINE-87053819; PubMed-2430793;

Pannekoek H., Veerman H., Lambers H., D.

van Zonneveld A.-J., van Mourik J.A.;

"Endothelial plasminogen activator inhil
the Serpin gene family."
EMBO J. 5:2539-2544(1986).
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PIR; S01324; S01324.
PIR; S06745; S06745.
HSSP; P01008; 1ATH.
                                                                                                                                                                                                                                                                                            PAII_HUMAN
P05121;
13-AUG-1987
13-AUG-1987
20-AUG-2001
PLASMINOGEN A
PLASMINOGEN A
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SEQUENCE
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ACT_SITE
CARBOHYD
CARBOHYD
CARBOHYD
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J. Cell Biol. 111:743-755(1990).

ACTIVATOR, UROKINASE, AND PROTEIN C. ITS RAPID INTERACTION WITH TPA MAY FUNCTION AS A MAJOR CONTROL POINT IN THE REGULATION OF FIBRINGLYSIS.

FIBRINGLYSIS.

J. Celli Biol. 111:743-755(1990).

J. Celli Biol. 111:743-75(1990).

J. Cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMAN
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                                                                                                                                                                                                                                                   13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
20-AUG-2001 (Rel. 40, Last sequence update)
21-AUG-2001 (Rel. 40, Last annotation update)
PLASMINOGEN ACTIVATOR INHIBITOR-1 PRECURSOR (PAI-1) (ENDOTHELIAL PLASMINOGEN ACTIVATOR INHIBITOR) (PAI).
SERPINEL OR PAI1 OR PLANHI.
HOMO Sapiens (Human)
                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                             Eukaryota;
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                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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|73 EEIIMD
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SIMILARITY: BELONGS TO THE SERPIN FAMILY.
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X52906; CAA37094.1;
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6; Conserv
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Lifity 100.0%;
Conservative
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REACTIVE BOND.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
S-1 L (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 29;
Pred. No.
                                                                                                                                                                                                         Craniata; Vertebrata; Catarrhini; Hominidae.
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                                                                                             Verweij C.L.,
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            SEQUENCE OF
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SEQUENCE (TO A SEQUENCE OF THE NUMBER OF THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    van Heerikhuizen H., Pannekoek H.;
"Structure of the human plasminogen
nonrandom distribution of introns.";
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Andreasen P.A., Riccio A., Welinder K.G., Douglas R., Sartorio R. Nielsen L.S., Oppenhelmer C., Blasi F., Dance K.; "Plasminogen activator inhibitor type-1: reactive center and amir terminal heterogeneity determined by protein and cDNA sequencing FEBS Lett. 209:213-218(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-86313660; PubMed-3092219; MY T., Sawdey M., Lawrence D., Millan J.L., Loskutoff D.J.; NY T., Sawdey M., Lawrence D., Millan J.L., Loskutoff D.J.; "Cloning and sequence of a cDNA coding for the human beta-migrating endothelial-cell-type plasminogen activator inhibitor."; Proc. Natl. Acad. Sci. U.S.A. 83:6776-6780(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. Cordes M., Doela D.; Submitted (JUN-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE-8900511; PubMed-3262512;

Strandberg L., Lawrence D., Ny T.;

"The organization of the human-plasminogen-activator-inhibitor-1

gene. Implications on the evolution of the serine-protease inhibitor
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X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS)
MEDLINE=92114970; PubMed=1731226;
                                                                                                                                                                                                                                                                                    TISSUE-Placenta;
MEDLINE-87105925; PubMed-3026837;
                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 17-402 FROM N.A., TISSUE-Placenta;
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Slightom J.L.;
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                                                                                                       VID T.C., Kretzmer K.K.;
"CDNA cloning and expression in E. coli of inhibitor (PAI) related to a PAI produced left. 210:11-16(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'Human plasminogen activator inhibitor-1
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263:9129-9141(1988).
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inders M., Keijer J., Veerman H.,
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en Berg E.A., Koolstra T.,
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Hep G2 hepatoma cell.";
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X-RAY CRYSTALLOGRAPHY (2.99 ANGSTROMS).
MEDLINE-99148119; PubMed=10386279;
Sharp A.M., Stein P.E., Pannu N.S., Carrell R.W.,
Ginsburg D., Lawrence D.A., Read R.J.;
The active conformation of plasminogen activator
target for drugs to control fibrinolysis and cell
structure 7:111-118(1999).
                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no restunse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Turkmen B., Schmitt M., Schmalfeldt B., Trommler P., Hell W., Creutzburg S., Gzaeff H., Magdolen V.;
"Mutational analysis of the genes encoding urokinase-type plasminogen activator (upA) and its inhibitor PAI-1 in advanced ovarian cancer.", Electrophoresis 18:686-689(1997).

1- FUNCTION: THIS INHIBITOR ACTS AS "BAIT" FOR TISSUE PLASMINOGEN ACTIVATOR, UROKINASE, AND PROTEIN C. ITS RAPID INTERACTION WITH
              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANT THR-15.
MEDLINE-97337920; PubMed-9194591;
Turkmen B., Schmitt M., Schmalfel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Interfering with the inhibitory mechanism of structure of a complex formed between cleaved inhibitor type 1 and a reactive-centre loop pestructure 6:627-636(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   x-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS).
MEDLINE-98298439; PubMed-9634700;
Xue Y., Bjorquist P., Inghardt T., Lins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aertgeerts K., de Bondt H.L., de Ranter C.J., Declerck P.J.; "Mechanisms contributing to the conformational and functional flexibility of plasminogen activator inhibitor-1."; Nat. Struct. Biol. 2:891-897(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mottonen J., Strand A., Symersky J., Sweet R.M., Danley Geoghegan K.F., Gerard R.D., Goldsmith E.J.; "Structural basis of latency in plasminogen activator in Nature 355:270-273(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                            FIBRINOLYSIS.

DISEASS: HIGH CONCENTRATIONS OF THIS PROTEIN HAVE
WITH HUMAN THROMBOEMBOLIC DISEASE.

MISCELLANEOUS: PAI1 IS INACTIVATED BY PROTEOLYTIC
UROKINASE-TYPE (U-PA) AND THE TISSUE-TYPE (TPA), C
                                                                                                                                                                                                                                                                                                                            MISCELLANEOUS: VASCULAR ENDOTHELIAL CELLS
OF SYNTHESIS OF PLASMA PAI.
SIMILARITY: BELONGS TO THE SERPIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                           369(R)-370(M) BOND.

MISCELLANEOUS: TWO TYPES OF PAI HAVE BEEN IDENTIFIED. PAI-1
ACID-STABLE GLYCOPFOTEIN FOUND IN PLASMA AND PLATELETS AND I
ENDOTHELIAL, HEPATOMA, AND FIBROSARCOWA CELLS.

MISCELLANEOUS: VASCULAR ENDOTHELIAL CELLS MAY BE THE PRIMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACTIVATOR, UROKINASE, AND PROTEIN C. ITS I
                                                                                                                                 X04429; CAA28025.1;

M14083; AAA60008.1;

X04729; CAA28438.1;

X04731; CAA28442.1;
                             M14083;
X04729;
X04731;
M16006;
M22314;
M22315;
M22315;
M22316;
M22317;
M22317;
                            AAA60009.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of serpins: crystal ed plasminogen activator peptide.";
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tent is in
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Matches 6
                                                                                                                                         SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-97206338; PubMed-9157595;
Bijnens A.P., Knockaert I., Cousin E.,
"Expression and characterization of reactivator inhibitor-1.";
activator inhibitor-1.";
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EMBL; X13340; CAB51737.1;
EMBL; X13341; CAB51606.1;
EMBL; X13342; CAB51607.1;
EMBL; X13343; CAB5139.1;
EMBL; X13343; CAB51739.1;
EMBL; X13344; CAB51739.1;
EMBL; X13345; CAA31729.1;
EMBL; X13345; CAA31729.1;
EMBL; X13764; AAA60007.1;
EMBL; X03764; CAA328444.1;
                                                                                                                                                                                                                                                                                                Sus scrofa (Pig).
Eukaryota; Metazoa; C
Mammalia; Eutheria; C
NCBI_TaxID=9823;
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P79335;
15-JUL-1998
15-JUL-1998
20-AUG-2001
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CARBOHYD
CARBOHYD
CARBOHYD
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update
PLASMINGEN ACTIVATOR INHIBITOR-1 PRECURSOR
PLASMINGEN ACTIVATOR INHIBITOR) (PAI).
SERPINE1 OR PAII OR PLANHI.
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Glycopr
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S02551; S02551.
9PAI; 19-MAR-99.
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Similarity 100.0%;
6; Conservative (
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CAA31722.1; -
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|ism; Signal;
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Pred. No. 12;
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f recombinant porcine
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CDA2 OR YLR307W OR L2142.2
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CARBOHYD
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Q06702;
                                                                                                                                          STRANN-S288C / AB972;
Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., D
Johnston M., Fulton L., Gattung S., Greco T., Kirsten J.,
Favello A., Fulton L., Gattung S., Hillier L., Jier M.,
Kucabb T., Hallsworth K., Hawkins J., Hillier L., Jier M.,
Johnson D., Johnston L., Langston Y., Latreille P., Le T.,
Mardis E., Menezes S., Miller N., Nann M., Pauley A., Pelus
Rifken L., Riles L., Taich A., Trevaskis E., Vignati D.,
Wilcox L., Wohldman P., Vaudin M., Wilson R., Waterston R.;
Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
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SMART;
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the Euro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities
                                       MEDIINE-97279228; PubMed-9133736; Mishra C., Semino C.E., McCreath Specht C.A., Robbins P.W.; Cloning and expression of two ch Saccharomyces cerevisiae.";
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              Yeast 13:327-336(1997)
                                                                                                                   CHARACTERIZATION.
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SIMILARITY: B
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UROKINASE-TYPE
 GLUCOSAMINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF00079; serpin; 1.
F; SM00093; SERPIN; 1.
ITE; PS00284; SERPIN; 1
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ilarity 100.0%;
Conservative
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Signal.
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WE RESIDUES
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402
370
232
288
352
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LONGS TO THE SERPIN FAMILY.
                                                                                                                                                                                                                                                                                                                            Saccharomycetaceae;
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precursor (EC 3.5.1.41).
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THE N-ACETAMIDO GROUPS OF N-ACETYL-D-IN CHITIN.
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PLASMINGER ACTIVATOR INHIBITOR-1.

REACTIVE BOND.

N-LINKED (GLCNAC. . .) (POTENTIAL).

MW; 13F60E5F4F8FE405 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                          Saccharomycotina;
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Mismatches
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Matches 5
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01-FEB-1995
01-OCT-1996
20-AUG-2001
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CARBOHYD
SEQUENCE
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                                                                                                                                                                                MEDLINE-97245296; PubMed-9090UDD; MEDLINE-97245296; PubMed-9090UDD; de Antoni A., D Angelo M., Dal Pero F., Sartorello Pallavicini A., Lanfranchi G., Valle G.; The DNA sequence of cosmid 14-13b from chromosome The DNA sequence of cosmid 14-13b from chromosome the Company of t
                                                                                                                                                                                                                                                                                                                                           MEDLINE-94237477; PubMed-8181746; MEDLINE-94237477; PubMed-8181746; Truan G., Epinat J.-C., Rougeulle C., Cullin C., Pompon D.; Truan G., Epinat J.-C., Rougeulle C., Cullin C., Pompon D.; Tcloning and characterization of a yeast cytochrome b5-encoding which suppresses ketoconazole hypersensitivity in a NADPH-P-450 reductase-deficient strain."; Gene 142:123-127(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- CATALYTIC ACTIVITY: CHITIN + H(2)O - CHITOSAN + AI
-i- DEVELOPMENTAL STAGE: EXPRESSED EXCLUSIVELY QURING
-i- SIMILARITY: TO OTHER POLYSACCHARIDE DEACETYLASES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fung1; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                            overlapping open reading frames.";
Yeast 13:261-266(1997).
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM
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STRAIN-FL100;
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                                 FUNCTION: CYTOCHRONE B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND OXYGENASES. IT PLAYS A ROLE IN FATTY ACID DESATURATION AND IS INVOLVED IN SEVERAL STEPS OF THE STEROL BIOSYNTHESIS PATHWAY, PARTICULARLY IN THE 4-DEMETHYLATION OF THE 4,4'-DIMETHYL
ZYMOSTEROL.
SUBCELLULAR
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$0004299; CDA2.
rpro; IPR002509; Polysac_deacet.
; PF01522; Polysac_deacet; 1.
clase; Chitin degradation; Signal;
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  MICROSOMAL
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Query Match
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Matches 5; Conserve
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2.69382.
2.791387; C.,
3.62; S47919; S47915.
3.62; S0005055; CYBS.
Interpro; IPRO01199; Cyt_B5.
Pfam; PF00173; heme_1; 1.
PROSITE; PS00173; CYTOCHROME_B5_1; 1.
PROSITE; PS00191; CYTOCHROME_B5_2; 1.
PROSITE; PS00255; CYTOCHROME_B5_2; 1.
PROSITE; PS00255; CYTOCHROME_B5_2; 1.
PROSITE; PS00255; CYTOCHROME_B5_2; 1.
PROSITE; PS00256; CYTOCHROME_B5_2; 1.
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PROSITE; PS00173; PS00173; PS00256; CYTOCHROME_B5_1; 1.
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PROSITE; PS00173; PS
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01-NOV-1995
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P42484;
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EMBL; Z69382; CAA93396.1; --
EMBL; Z71387; CAA95990.1; --
PIR; S47919; S47919.
HSSP; P04166; LB5M.
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                                                                                                                                                                                                                                                                                                                                                                  Virology 208:249-278(1995).

-I: FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS SUBSTRATES.
-I: CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE - N PYROPHOSPHATE +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yanez R.J., Rodriguez J.M., Nogal M.L., Yuste L., Enriquez C., Rodriguez J.F., Vinuela E.;
"Analysis of the complete nucleotide sequence of African swine fever
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           African swine fever virus (strain BA71V) (ASFV).
Viruses; dsDNA viruses, no RNA stage; Asfarviridae;
African swine fever-like viruses.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM
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41 DEIIMD 46
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                                                                                                                                                                                                                                                                                                                                             RNA(N)
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32, Last sequence update)
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E -> Q (IN REF. 1).
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598EF2A6730CAD19 CRC64;
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                                                                                                                                                            It is produced through a collaboration
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YE95_METJA
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Best Local S
Matches 5
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Best Local Similarity 83.3
Matches 5; Conservative
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MEDLINE-96337999; PubMed-8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus Jannaschil.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997
01-NOV-1997
20-AUG-2001
                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, U18465, AAA65299.1; -.
InterPro; IPRO01725; RNA_POIK_14KD.
Pfam; PF01192; RNA_POI_K; 1.
PROSITE; PS01111; RNA_POI_K, 14KD; 1.
Transferase; DNA-Glirected RNA polymerase; Transcription.
SEQUENCE 147 AA; 16691 MW; 6D0B66D77025CD45 CRC64;
                                                                                                                                 Hypothetical protein; Transmembrane; Complete proteome
TRANSMEM 17 37 POTENTIAL.
SEQUENCE 292 AA; 33508 MW; B8A34C29B3A51246 CRC64;
                                                                                                                                                                                                       EMBL; U67590; AAB99506.1; -. TIGR; MJ1495; -.
                                                                                                                                                                            InterPro; IPR002825; DUF114. Pfam; PF01972; DUF114; 1.
                                                                                                                                                                                                                                                                                                                                                                        Science 273:1058-1073(1996).
-1- SIMILARITY: STRONG, TO M.JANNASCHII MJ0137.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Archaea; Euryarchaeota;
Methanococcus.
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| EDIIMD 12
                              EEIIMD 6
                                                          Similarity 83.
5; Conservative
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(Rel. 35, Last sequence up
(Rel. 40, Last annotation
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83.3%;
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                                                         Score 26; DB Pred. No. 45; 1; Mismatches
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Pred. No.
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                                                                                                                                                               Complete proteome
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RESULT
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Best Local S
Matches 5
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20 STRAIN=RD / KW20 / ATCC 51907;

21 X MEDLINE=95350630; PubMed=7542800;

22 X MEDLINE=95350630; PubMed=7542800;

23 Fleischmann R.D. Adams M.D. White O., Clayton R.A., Kirkness E.F.,

24 Kerlavage A.R., Bult C.J., Tomb J-F., Dougherty B.A., Merrick J.M.,

25 Kerlavage A.R., Sutton G., Fitzhugh M., Fields C.A., Gocayne J.D.,

26 Kerlavage A.R., Sutton G., Fitzhugh M., Fields C.A., Gocayne J.D.,

27 Weldman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

28 Weldman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

29 Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

20 Kanna J.L., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

29 A Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,

20 Venter J.C.;

21 Whole-genome random sequencing and assembly of Haemophilus

21 Tinfluenzae Rd.*;
                                                                                                                                                                                                       YLN9_CAEEL
Q09512:
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01-NOV-1995 (Rel. 3
20-AUG-2001 (Rel. 4
MU-LIKE PROPHAGE FI
                                                                                                                              009512;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL 76.7 KDA PROTEIN D2013.9 IN CHROMOSOME
D2013.9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
SEQUENCE FROM N.A. STRAIN-BRISTOL N2; Mortimore B., Matt
                                                                             Caenorhabditis elegans.
Eukaryota; Metazoa; Nematc
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein; Complete SEQUENCE 508 AA; 57190 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U32826; AAC23150.1; -. TIGR; HI1500; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           influenzae Rd.";
Science 269:496-512(1995).
-1- SIMILARITY: STRONG, TO PHAGE MU PROTEIN GP28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haemophilus
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Proteobacteria;
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32, Last sequence update)
40, Last annotation update)
FLUMU PROTEIN GP28.
                                                                                 Nematoda; Chromadorea; Rhabditida; Rhabditoidea; rinae; Caenorhabditis.
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5BFC6833E2F1242B CRC64;
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84;
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RESULT 12
Y961_METJA
ID Y961_METJA
AC Q58371;
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Best Local S
Matches 5
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EMBL; 247809; CAA87778.1; ---
EMBL; 247809; CAA87783.1; ---
EMBL; 247808; CAA87783.1; JOINE
WORMPEP; D2013.9; CE01535
InterPro; IPR001214; SET:
IPR0SITE; PS50280; SEP; 1.
Hypothetical protein;
SEQUENCE 662 AA; 76750 MW;
                                                                                                                                                                                                                                                     STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE-96337999; PubMed-8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997
01-NOV-1997
20-AUG-2001
                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Methanococcus jannaschii.
Archaea: Euryarchaeota: M
Methanococcus.
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-!- SIMILARITY: STRONG, TO HUMAN KIAA0153.
               EMBL; U67539; AAB98963.1; TIGR; MJ0961; -.
                                                                                                                                                                                                                      Science
                                                                                                                                                                                                                                     "Complete genome sequence jannaschii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL
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5; Conserv
                                                                                                                                                                                           273:1058-1073(1996).
ILARITY: BELONGS TO THE MCM FAMILY.
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(Rel. 40, Last annotation
L MCM-TYPE PROTEIN MJ0961.
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Pred. No. 1.1e+02;
1; Mismatches (
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IPR001208; MCM.

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RESULT 13
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3EQUENCE FROM N.A.
STRAIN-K12 / MC1655;
MEDLINE-97426617; PubMed-9278503;
Blatther F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Blatther F.R., Punkett G. III, Bloch C.K., Mayhew G.F.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YHGF_ECOLI STA
P46837; P76689;
01-NOV-1995 (Rel.
15-JUL-1999 (Rel.
20-AUG-2001 (Rel.
     CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IDENTIFICATION BY MASS SPECTROMETRY.

MEDLINE-99420866; PubMed-10,493123;
Fountoulakis M, Takacs M.-F., Berndt P., Langer
"Enrichment of low abundance proteins of Escheri
hydroxyapatite chromatography.";
Electrophoresis 20:2181-2195(1999).
-1- SIMILARITY: STRONG, TO H.INFLUENZAE H10568.
-1- SIMILARITY: CONTAINS 1 'S1 MOTIF' DOMAIN.
                                                                                                                                                                                    EMBL; U18997; AAA58204.1; ALT_FRAME. EMBL; U18997; AAA58205.1; ALT_FRAME. EMBL; AE000416; AAC76432.1; ALT_INITHSSP; P05055; 1SRO.
                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long, as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-s or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00847; MCM_1; 1.

PROSITE; PS50051; MCM_2;

Hypothetical protein; Transcription regulation; DNA-binding;

DNA replication; Cell cycle; MTP-binding; Complete proteome.

DOMAIN 34 542

NP_BIND 384 391

NP_BIND 384 391

ATP (POTENTIAL).

SEQUENCE 762 AA; 87526 MW; 3323509057464C12 CRC64;
RNA-binding; Complete proteome.

DOWAIN 651 720

CONFLICT 754 755

SEQUENCE 773 AA; 85119 MW; EA54D9ED952A8229 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli
Bacteria; Proteobacteria;
                                                                                                                    EcoGene; EG12932; yhgf.
InterPro; IPR003029; S1.
Pfam; PF00575; S1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=562;
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SMART; SM00350
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Q08399;
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Q1-NOV-1997
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Azeddoug H., Reysset G.;
Cloning and sequencing of a chromosomal fragment from a cetobutylicum strain ABKn8 conferring chemical-damagin UV resistance to E. coli recA strains.*;
Curr. Microbiol. 29:229-235(1994).
-1- FUNCTION: NOT KNOWN; COULD CONFER METHYL METHANE SU MITOMYCIN C (MC), AND UV RESISTANCE.
-1- SIMILARITY: BELONGS TO THE CAPAB / TERDEXZ FAMILY.
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15-JUL-1999 (Rel. 3
15-JUL-1999 (Rel. 3
CHEMICAL-DAMAGING A
African swine fever virus (isolate Malawi Lil 20/1) (ASFV). Viruses; dsDNA viruses, no RNA stage; Asfarviridae; African swine fever-like viruses. NCBI_TaxID-10500; [1]
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Pfam; PF0
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Q45811;
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Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
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NCE 139 AA; 15429 MW;
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POLYMERASE, SUBUNIT 6 HOMOLOG (EC 2.7.7.6).
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AGENT RESISTANCE PROTEIN B.
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RX MEDILINE-9332438; pubMed-8332503;
RX MEDILINE-9332438; pubMed-8332503;
RY An African swine fever virus gene with a similarity to eukaryotic RT An African swine fever virus gene with a similarity to eukaryotic RT RNA polymerase subunit 6; respectively a succience Acids Res. 21:2940-2940(1993).
CC -1- FUNCTION: DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS CC -1- CAPALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE - N PYROPHOSPHATE + CRANLYN; RNA POLYMERASE SUBUNIT FAMILY.
CC RNA NIN; RNA POLYMERASE SUBUNIT FAMILY.
CC RNA POLYMERASE SUBUNIT FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation.
CC the European Bloinformatics Institute. There are no restrictions on its cuse by non-profit institutions as long as its content is in no way non-profit institutions as long as its content is in no way non-profit institutions as long as its content is in no way non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercial considerable and this statement generous (see http://www.isb-sib.ch/announce/C or send an email to licensedish-sib.ch).
CC Interpro, IPRO0172: RNA_POLK_14KD.
CC RMB; LISALI, AAA42731.1; RNA_POLK_14KD.
CC RMB; LISALI, AAA42731.1; RNA_POLK_14KD.
CC RMB; LISALI AAA42731.1; RNA_POLK_14KD.
CC RMB; LISALI AAA42731.1; RNA_POLK_14KD.
CC RMB; Length 139;
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Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Search completed: March 18, 2002, 09:52:26
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## ALIGNMENTS

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O51223 PRELIMINARY; PRT;
O51223;
O1-JUN-1998 (TrEMBLrel. 06, Created)
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STRANN-CV. COLUMBIA;
Rounsley S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M.,
Shen M., Ronning C.M., Fraser C.M., Somerville C.R., Venter J.C.;
"Arabidopsis thaliana chromosome II BAC T30L20 genomic sequence.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AC00517; AAC63587.];
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InterPro; IPR001092; HLH_dim.
Pfam; PF00010; HLH; 1.
SMARR; SM00353; HLH; 1.
SMARR; SM00353; HLH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01.NOV-1998 (TREMBLrel 08, Created)
01.NOV-1998 (TREMBLrel 08, Last sequence update)
01.NOV-101 (TREMBLREL 17, Last annotation update)
11.TUN-2001 (TREMBLREL)
12.6 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                          Score 29; DB Pred. No. 73;
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Q9HHB1;
01-MAR-2001
01-MAR-2001
01-JUN-2001
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STRAIN-ANCC 35210 / B31;

MEDLINE-98065943; PubMed-9403685;

Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.,
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K.,
Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Ha
van Vut R., Palner N., Adams M.D., Gocayne J.D., Weidman J.
Utterback T., Watthey L., McDonald L., Antlach P., Bowman C.
Garland S., Fujll C., Cotton M.D., Horst K., Roberts K., Hat
Smith H.O., Venter J.C.;
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Nature 390:580-586(1997).
EMBL; AE001131; AAC06601.1; ...
TIGR; BB0205; ....
                                                                                                                                                                                                                                                                                                Submitted (OCT-1999) to the EMBL/GenBank/DDBJ database EMBL; AF197899; AAG28517.1; -
Interpro; IPRO02316; trNA-synttpro.
PRINTS; PRO1046; TRNASYNTHPRO.
Aminoacyl-trNA synthetase; Ligase.
SEQUENCE 460 AA; 53292 MW; DAB364435B808E44 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                "A single class II synthetase specifies two translation.";
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Stathopoulos C., Li T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLRel. 17, Last annotation update)
PROLYL-TRNA SYNTHETASE (EC 6.1.1.15).
Methanococcus maripaludis.
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Similarity 100.0%;
6; Conservative 0;
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83.3%;
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Spirochaetaceae; Borrelia
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1; Mismatches
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Pred. No. 1.4e+02;
Mismatches 0;
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837F0B2A35EB255D CRC64;
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y E.K., Gwinn M.,
n D.,
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MEDINE-21173698; pubMed=11259647;

Mierman W.C., Feldblyum T.V., Laub M.T., Ohta N., Maddock J.R., Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Potocka I., Welson W.C., Newton A., Stephens C., Phadke N.D., Ely B. DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Barry K., Utterback T., Tran K., Wolf A., Vanathevan J., Ermolaeva M., White Callberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

"Complete genome sequence of Caulobacter crescentus.";

Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

EMBL; AE006028; AAK25672.1;

"TIGR, CC3710;

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01-MAR-2001 (TREMBLIEL. 16, Last sequence update)
01-UN-2001 (TREMBLIEL. 17, Last annotation updat
GENOMIC DNA, CHROMOSOME 5, TAC CLONE:K18P6.
                                                                      EMBL; AB010068; BAB11210.1; -.
Interpro; IPR001934; HMA.
Interpro; IPR001230; Prenyltn.
Pfam; PF00403; HMA; 2.
                                                                                                                                                                                                                      "Structural analysis of Arabidopsis thallana chromosome 5. IV. Sequence features of the regions of 1,456,315 bp covered by nineteen physically assigned pl and TAC clones."; DNA Res. 5:41-54(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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SEQUENCE 12
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                                                                                                                                                                                                                                                                                                                                                                               Tabata S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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120 AA; 12483 MW; B30E9BCA06F9283A CRC64;
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        PRENYLATION; UNKNOWN_1.

; 35350 MW; 5A97CA58833BCDE0 CRC64;
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OSLJIJ3 PRELIMA....

OSLJIJ3 PRELIMA....

OSLJIJ3;

O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)

O1-OCT-2000 (TrEMBLrel. 15, Last annotation update)

O1-OCT-2000 (TrEMBLrel. 15, Last annotation update)

ZINC METALLOPROTEASE (INSULINASE FAMILY).

Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyjedons; core eudicots; Rosidae;

ceurosids II; Brassicales; Brassicaceae; Arabidopsis.
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EMBL; ALO32644; CAA21671.1; -.
InterPro; IPRO00922; Znf-C2H2.
Pfam; PF00096; Zf-C2H2; 1.
SMART; SM00355; ZnF-C2H2; 1.
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laiteter N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen J
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00028; ZINC_FINGER_C2H2_1;
PROSITE; PS50157; ZINC_FINGER_C2H2_2;
DNA_binding; Zinc-finger;
DNA_binding; Zinc-finger;
SEQUENCE 574 AA; 65776 MW; 9146676
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Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
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9 (TrEMBLrel. 12,
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2; Mismatches
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4.6e+02;
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Altawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Kalota K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaldo I., Pesole G., Quackenbush J.,
RA Fleischmann M., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaldo I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Blake J., Boidelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Blake J., Boidelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Filita M., Gariboldi M.,
RA Brownstein M.J., Bult C., Fletcher C., Filita M., Gariboldi M.,
RA Hyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA RA Wordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Suzuki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Sato K., Schoenbach C., Seya T., Shibata Y., Kontsuki S.,
RA Havashizaki Y...
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Q9CQW6;
01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
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DNA Res. 7:217-221(2000).
EMBL: AP000419; BAB02957.1;
                                                                                                                                                                                                       *Functional annotation of a full-length mouse cDNA collection.*;

Nature 409:685-690(2001).

EMBL; AK006646; BAB24686.1; -.

EMBL; AK0066418; BAB24578.1; -.

MGD; MGI:191433; 1700027H16Rik.

SEQUENCE 152 AA; 17571 MW; 4DE5F01744ED1E58 CRC64;
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PubMed-10907853;
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Kaneko T., Kato T.,
Submitted (SEP-1999)
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1700027H16RIK PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hayashizaki Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21085660; PubMed=11217851;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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5; Conservative
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Rodentia;
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                                      89.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17,
17,
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Last sequence update)
Last annotation update)
Score 26; DB 11;
Pred. No. 1.9e+02;
1; Mismatches 0;
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Pred. No. 8.7e+02;
1; Mismatches 0
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Sciurognathi; Muridae;
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                                                                                  Length 152;
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; Murinae; Mus
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RA KAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Kadota K., Matsuda H.A, Ashburner M., Batalov S., Casavant T.,
A Kadota K., Matsuda H.A, Ashburner M., Batalov S., Casavant T.,
A Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuchi P., Lewis S., Matsuo Y., Nikaido II., Pesole G., Quackenbush G.,
A Kuchi P., Lewis S., Matsuo Y., Nikaido II., Pesole G., Quackenbush G.,
A Kuchi P., Lewis S., Matsuo Y., Nikaido II., Pesole G., Quackenbush G.,
A Schriml L.K., Staubli F., Suzuki R., Tomita M., Magner L., Washio T.,
A Schriml L.K., Staubli F., Suzuki R., Tomita M., Magner L., Washio T.,
A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
A Brownstein M.J., Bult C., Klandann M., Hume D.A., Kamiya M., Lee N.H.,
A Hordone P., Warchonni L., Mashima J., Mazzarelli J., Mombaerts P.,
A Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
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Best Local
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Q9D385;
Q1-JUN-2001
01-JUN-2001
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
6330544B05RIK PROTEIN (SIMILAR TO BINDER OF ARL TWO).
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09Y2YO;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ARF-LIKE 2 BINDING PROTEIN BART1 (BINDER OF ARL TWO).
Homo sapiens (Human)
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-C578L/6J; TISSUE-MEDULLA OBLONGATA;
MEDLINE-21085660; Pubmed-11217851;
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Submittled (FEB-2001) to the
EMBL; AR126062; AAD20633.1;
EMBL; BC003087; AAH03087.1;
SEQUENCE 163 AA; 18822 M
                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
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"The Arf-like 2 (Ari2) binding protein BART1: purification, cloning, and initial characterization.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
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29 EDIIMD 34
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                                                                                                                                                                                                                                                                                                                                                                                   Chordata;
Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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2.1e+02;
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Rasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Gariboldi M.,
RA Brownstein M.J., Bult C., Fletcher C., Fulita M., Gariboldi M.,
RA Brownstein M.J., Bult C., Fletcher C., Fulita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kmiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Hayashizaki Y., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.,
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Matches 4
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Best Local S
Matches 5
                                                                                                                                                           Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA col
"Functional annotation of a full-length mouse cDNA col
Nature 409:685-690(2001).
EMBL; AKO06511; BAB24626.1; -
MGD; MGI:1916746; 1700029M23Rik.
SEQUENCE 175 AA; 20552 MW; 15AEB6A38F87706E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-057BL/6J; TISSUB-TESTIS;
MEDLINE-21085660; PubMed-11217851;
MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.; Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
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01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
1700029M23RIK PROTEIN.
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Submitted (J
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5; Conser
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                               89.7%;
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83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation updat
   Score 26; DB 11;
Pred. No. 2.2e+02;
2; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                          mouse cDNA collection.";
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                                                                   Length 175;
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                                                                                    RESULT
Q9F0U6
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Best Local S
Matches 5
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Q9F0U6;
Q9F0U6;
01-MAR-2001
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NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-BONE MARROW:
Zhao M., Gu J., Li N., Peng Y., Han Z., Chen Z.;
Zhao M., Gu J., Li N., Peng Y., Han Z., Chen Z.;
*A novel gene expressed in human bone marrow. *;
*Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
SEMBL, AF217515, AAR67626.1;
*SEQUENCE 204 AA; 24053 MH; 39E4E5F78E020260 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Harrison L.M., Cappello M.;
"Isolation of a cathepsin b-like sequence from adult Ancylostoma
ceylanicum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID-9606;
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01-OCT-2000 (TremBLrel. 15,
01-OCT-2000 (TremBLrel. 15,
UNCHARACTERIZED BONE MARROW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Signal.
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
Ancylostomatoidea; Ancylostomatidae; Ancylostomatinae; Ancylostoma.
NCBI_TaxID-53326;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CATHEPSIN B-LIKE PRECURSOR PROTEIN (FRAGMENT).
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180 AA;
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   (TrEMBLrel. 16,
                                                            PRELIMINARY;
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20099 MW; · F3729B7CC683E601
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Last sequence update)
Last annotation update)
PROTEIN BM039.
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Pred. No. 2.3e
2; Mismatches
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                               DB 4;
2.6e+02;
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SQUEDE RELEASE OF THE PROPERTY OF THE PROPERTY
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Best Local S
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"Sequence of o-chlorophenol reductive dehalogenase from
"Desulfitchacterium chlororespirans Co23.";

Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

R EMBL; AP204275, AAG43484.1;

R InterPro; IPR001808; HTH_CRP.
InterPro; IPR001808; HTH_CRP.
INTERPRO; SMO0109; CNMP-J.

R SMART; SM00109; CNMP-J.

R SMART; SM00109; CNMP-BINDING_3; 1.

R SMART; SM00419; HTH_CRP. 1

R SMART; SM00419; HTH_CRP
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Best Local Similarity 83.7
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          Complete
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-96344137; PubMed-9679194;
KAWATADAYAS1 Y., Sawada M., HOTIKAWA H., HAIKAWA Y., HINO Y.,
YAMAMOTO S., Sekine M., Baba S.-I., Kosuqi H., Hosoyama A., Nagai !
Yamamoto S., Sekine M., Baba S.-I., Kosuqi H., Takamiya M., Ohfuku Y.,
Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
Yunahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi
Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
Masuchi Y., Shizuya H., Kikuchi H.;
Masuchi Y., Shizuya H., Kikuchi H.;
Masuchi Y., Sequence and gene organization of the genome of a hyper-
thermophilic archaebacterium, Pyrococcus horikoshii OT3.*;
DNA Res. 5:55-76(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     059224
059224;
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01-JUN-2001 (TEMBLEel. 17, Last annotation update)
HYPOTHETICAL 26.9 KDA PROTEIN.
Desulfitobacterium chlororespirans.
Bactleria; Firmicutes; Bacillus/Clostridium group;
Hellobacterium group; Desulfitobacterium.
NCBL_TaxID-51616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN-OT3;
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Archaea; Euryarchaeota;
NCBI_TaxID=53953;
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AUG-101 (TrEMBLrel. 17, Last annotation update)
274AA LONG HYPOTHETICAL AUTOANTIGEN LIKE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-CO23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001247; 3_ExoRNase.
Pfam; PF01138; RNase_PH; 1.
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213 EELVMD
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                                                                                                                                                                         Similarity 66. 4; Conservative
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274 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                               29994 MW;
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Search completed: March 18, 2002, 09:51:57 Job time: 286 sec

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Result
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                                                                                                                                                                                                                                                                                    Score
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Match
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29
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Gapop 10.0 , Gapext 0.5
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AAR07245
AAR23812
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AAY72392
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                                                      AAR83032
AAY33889
                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
Peptide used to re PAI-1(E350-PR). H PAI-1 (ARG 350) mu H. pylori GHPO 103 Pyrenophora teres Shrimp white spot Corn LHT1 encoded Polypeptide encode Amino acid sequenc Neisseria meningit
                                                                                                                                                                                                                                                                                    Description
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5	44	3	42	41	40	39	38 8	37	36	35	34	ω u	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12
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AAY69860		6985	985	85	35	5	39	39	39	AAB78388	AAB78387	AAB78386	AAY90001	AAY89998	AAY89994	AAY89993	AAY89987	AAY89986	AAY89985	AAB92200	AAY42738	AAY01812	AAB23601	930	935	272	AAB69050		443	176	0863	607	AAR21412
FIV gp36 envelope	IV gp36 enve	gp36	gp36	gp36	FIV gp36 envelope	e polypeptide		tide	ide	polypeptide	polypeptide	tide	ptide	polypept	ore polypeptide	tide	polypeptide	polypeptide		ibito	-an	к	secret	Human BAI3 protein	ebacte	C glutamicum prote	ribonucl	protein	ĕ	Streptococcus pneu	Amino acid sequenc	S. pneumoniae deri	NADH dehydrogenase

# ALIGNMENTS

RESULT 1 AAY01813

29-JUN-1999

(first entry)

AAY01813;

AAY01813 standard; peptide; 6 AA

Peptide used to regulate scuPA.

scuPA clearance;

Abnormal cell migration; PAI-1-dependent cell adhesion; scuPA clearance pathological cell migration; angiogenesis; organogenesis; ovulation; inflammation; cancer; tumor cell invasion; metastasis; atherosclerosis. Example 1; Page 31; 63pp; English. Peptide composition WPI; 1999-288168/24. Cines D, (UYPE-) UNIV PENNSYLVANIA. 17-0CT-1997; 15-OCT-1998; 29-APR-1999 WO9920295-A1. Synthetic. Higazi AA; 97US-0062274 98WO-US21800

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The sequence represents AAs 1-380 of the PAI-1 protein chain.

The mutant was obtd. by site directed mutagenesis of the wild type gene. It has an Arg at posn. 350 replacing the Glu residue which is thought to form a contact with the t-PA Arg residue at posn. 304. The binding is modelled on that of the complex formed between tryps in and BpTI where the Tyr39 of trypsin forms a Van der Waal's contact with Ile19 of BPTI. In the mutant the Glu residue has been replaced by and Arg residue, restoring the electrostatic interaction that was disrupted by the construction of the Arg304-> Complementary to the mutant t-PA. The mutant serpin is a more active inhibtor than its parent protein.
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Best Local S
Matches 6
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                                                                                                                                                                                                                                                                                                                                                                       Serine protease mutant of the chymotrypsin super-family compsn. including it and genes encoding it, resistant to inhibition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-NOV-1989;
06-MAR-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tissue plasminogen activator; light chain; mutant; serine protease; chymotrypsin; salt bridge; serpin; inhibitor; t-PA.
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nilarity 100.
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89US-0319212
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ches 0;
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Best Local S
Matches 6
Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 6; Conservative (
                                                                          This PAI-1 mutant has Glu 350 of wild-type mature PAI-1 substituted by Arg. This substitution was chosen to selectively alter the negatively-charged Glu residue to a positively-charged Arg residue and promote potential interactions with the negatively charged Glu 304 residue in the PAI-1-resistant tPA mutant tPA(Glu304) (see AAR23804). The mutant PAI-1 showed an increased rate constant of interaction with tPA(Glu304) c.f. wild-type PAI-1. The sequence given as AAR23813 does not appear in the specification but has been compiled from the known PAI-1 sequence (see WO9013648) and the description given in the specification.
                                                                                                                                                                                                                                  New zymogen plasminogen activator mutants - inhibition by cognate serpin inhibitors in for myocardial infarction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tissue plasminogen activator; mutant; serine protease; zymogen-like; PAI-1; plasminogen activator inhibitor; coagulation; chymotrypsin superfamily.
                                                       Sequence
                                                                                                                                                                                                             Example 2; Page 55; 82pp; English.
                                                                                                                                                                                                                                                                                WPI; 1992-150888/18
                                                                                                                                                                                                                                                                                                       Gerard RD,
                                                                                                                                                                                                                                                                                                                                                   28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                        10-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein
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/label- mature_PAI-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                leader
                                                                                                                                                                                                                                                                                                       Goldsmith EJ,
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Score 29; DB
Pred. No. 43;
0; Mismatches
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Pred. No. 41;
); Mismatches
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          DB
43;
                                                                                                                                                                                                                                                                                                       Madison
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    resistant
plasma and

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                      13:
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                      Length 402;
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                                                                                                                                                                                                                                                                                                       Sambrook JF;
                                                                                                                                                                                                                                              platelets,
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RESULT
AAW98747
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                                                                        RESULT
                                                                                                                                                Matches
                                                                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JUL-1997;
01-APR-1997;
24-JUN-1997;
                                                                                                                                                                                                                      This sequence represents a Helicobacter pylori GHPO protein of the invention. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroduodenal diseases associated with these infections, including acute, chronic, and atrophic gastritis, and peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also be used for the production of antibodies. The products can also be used for the production of antibodies.
          12-SEP-2001
                              AAU03391;
                                                                                                                                                                                                                                                                                                             Claim 8; Page 1594-1596; 2054pp; English
                                                                                                                                                                                                                                                                                                                               New isolated Helicobacter polynucleotides for the diagnosis, prevention and treatment infections and gastrointestinal diseases
                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-542293/46.
N-PSDB; AAX14466.
                                                                                                                                                                                                                                                                                                                                                                                                          Al-Garawi A,
                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC.
(INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          \ensuremath{\mathsf{GHPO}} protein; \ensuremath{\mathsf{Helicobacter}} infection; \ensuremath{\mathsf{gastrodu\'odenal}} disease; \ensuremath{\mathsf{gastritis}} peptic ulcer disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H. pylori GHPO 1033 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAR-1999 (first entry)
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                                                   AAU03391 standard;
                                                                                                      1 REIIMD 6
|||:||
270 reilmd 275
                                                                                                                                                                                                   Sequence
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                                                                                                                                                Local Similarity
nes 5; Conserv
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                                                                                                                                                 Conservative
         (first
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97US-0833457.
97US-0881227.
                                                                                                                                                                                                     AA;
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                                                    Protein;
          entry)
                                                                                                                                                          93.1%;
                                                    758
                                                                                                                                                          Score 27;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                          Miller C,
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                                                                                                                                                  Mismatches
                                                                                                                                                                     DB 19;
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les 0;
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of Helicobacter
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                                                                                                                                                                     Length 340;
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AAG85015
ID AAG8
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AC AAG8
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           11-SEP-2001
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Query Match
Best Local S
Matches 4
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                                                                                                                                                                                                                                                                        Claim 24; Page 39; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CPS1; peptide synthetase; peptide toxin; fungal pathogen; corn crop infection.
                    AAG85015;
                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                       N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                          23-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pyrenophora teres.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pyrenophora teres partial CPS1 peptide synthetase
                                     AAG85015 standard;
                                                                                                                                                                                                                                                                                         New isolated nucleic acid molecule from a plant pathogen useful preventing plant pathogenic infections -
                                                                                                                                                                                                                                                                                                                                                   Yoder OC,
                                                                                                                                                                                                                                                                                                                                                                      (CORR ) CORNELL RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                            22-NOV-2000;
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                                                                                     328 revvmd
                                                                                                      1 REIIMD 6
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DB; AAS06685.
                                                                                                                           4:
                                                                                                                                   Similarity
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                                                                                                                                                                          758 AA;
                                                                                     333
                                                                                                                           Conservative
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(first entry)
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524..543
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221..2
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217..225
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755..70
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/note= "Peptide synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note "Peptide synthetase motif,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                    ,
28
                                      Protein; 1245
                                                                                                                                   93.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Peptide synthetase motif,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Peptide synthetase motif,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Cyclization domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Peptide synthetase
                                                                                                                                                                                                                                                                                                                                                    Ę
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                                                                                                                           Score 27; DB
Pred. No. 2.5e
2; Mismatches
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                                      A
                                                                                                                           DB 22; I
2.5e+02;
hes 0;
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                                                                                                                                            Length 758;
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RESULT
AAY72392
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                     26-DEC-2000
                                                      US6165792-A.
                                                                                                                        Corn; lysine- and histidine-specific transporter;
proline transporter; transgenic plant; immunologic
                                                                                                                                                                          Corn LHT1 encoded by cDNA clone ctaln.pk0048.h2
                                                                                                                                                                                                                                                                                AAY72392 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primary nucleotide sequence of the shrimp white spot Bacilliform virus (WSBV), useful for producing viral polypeptides that can be used to screen for agents that are useful for treating WSBV infection -
                                                                                       2ea mays.
                                                                                                                                                                                                               24-APR-2001
                                                                                                                                                                                                                                                 AAY72392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Figure 3; 626pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xu X, Yang F, He J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PENY-) PE CORP NY.
(THIR-) THIRD INST OCEANOGRAPHY STATE OCEANI C
(SINO-) SINOGENOMAX CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-NOV-2000; 2000WO-US28888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      White spot syndrome virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shrimp white spot Bacilliform virus; WSBV; diagnosis; viral infection; antiviral agent; gene expression; antisense construct; transgenic viral resistant shrimp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shrimp
                                                                                                                                                                                                                                                                                                                                                                      792 relimd 797
                                                                                                                                                                                                                                                                                                                                                                                                      1 REIIMD 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 83.:
5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1245 AA;
                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             spot Bacilliform virus (WSBV) protein 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99CN-0124717.
                                                                                                                                                                                                                                                                                Protein; 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                         93.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pham
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 27; DB
Pred. No. 4.1e
1; Mismatches
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                                                                                                                        cliic transporter; LHT1;
plant; immunological screening
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RESULT

AAR83032

ID AARR

XX AAR8

AC AAR8

AC CAP8

KW CAP9

KW CEP8

KW SEFC

XX STFG

XX W09!

PN W09!

PN W09!

PN W109!

PN W109!
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Best Local
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                   (UABR-) UAB RES FOUND
                                                                                     16-MAY-1995;
                                                                                                                        23-NOV-1995
                                                                                                                                                          WO9531548-A1
                                                                                                                                                                                           Streptococcus
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246 rqiimd
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The invention relates to lysine and histidine-specific transporter CC (LITH), proline transporter and their corresponding cDNA clones. It is useful for producing transgenic plants with altered expression level of camino acid transporters, in cell types or developmental stages in which corresponding transporters, and the obtained transgenic plants of they are not normally found, such that the obtained transgenic plants can be in cells of the transgenic plant, is also altered constitution and proline in cells of the transgenic plant, is also altered. The invention is also used for constructing a chimeric gene encoding all corresponding to the amino acid transporter, where in the expression of chimeric gene results in the production of altered levels of amino acid transporter in a transformed host cell. Synthetic peptides obtained from the corresponding transporter are used for immunising animals to produce polyclonal or monoclonal antibodies, which facilitates the immunological screening of cDNA expression libraries.
                                                                                                                                                                                                    Capsular polysaccharide; cps; peptide; flanking region; detection; serotype; diagnosis; prevention; Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding amino acid transporters, e.g. lysine- and histidine-specific transporter and proline transporter, useful for transgenic plant production with altered expression level of the amino acid transporters
                                                                                                                                                                                                                                                                  Polypeptide encoded by 5' flanking region of cps gene
                                                                                                                                                                                                                                                                                                                                                                                           AAR83032 standard; peptide; 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is corn lysine and histidine specific transporter (LHT1) from clone ctaln.pk0048.h2, isolated from a corn tissue ctaln CDNA library.
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N-PSDB; AAD02471.
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nes 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       259 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                             pneumoniae.
94US-0243546
                                       95WO-US06119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89.7%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 26; DB
Pred. No. 1.4e
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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AAY33889
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Best Local S
Matches 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                infection; bacterial capsule; serotype specific; virulence; diagnosis; capsule synthesis; cassette model; blnary model; cassetting-in; flanking region; non-serotype specific.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New Streptococcus pneumoniae capsular polysaccharide genes for detection, serotyping and for diagnosis and prevention pneumoniae infection
                                                                                      Non-serotype-specific flanking nucleotide sequences derived from Streptococcus pneumoniae capsular polysaccharide genes, useful as hybridization probes for identifying serotype-specific capsular polysaccharide genes
                                                                                                                                                                                                                                                                                    02-JUN-1997;
16-MAY-1994;
                                                                                                                                                                                                                                                                                                                                      02-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                     07-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                     US5948900-A
                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid sequence of Cps3B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY33889 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Page 166; 226pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dillard JP,
                                                                                                                                                                        WPI; 1999-517979/43.
N-PSDB; AAZ11798.
                                                                                                                                                                                                                       Dillard J, Yother J;
                                                              Claim
Serotype-specific cps genes encode the
                              This is is the amino acid sequence of the capsule synthesis
                                                                                                                                                                                                                                                    (UABR-) UAB RES FOUND.
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|:||||
52 rkiimd 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pneumoniae infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1996-010934/01.
DB; AAT05485.
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5; Conserv
                                                              Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yother
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                             6a; 140pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                    pneumoniae.
                                                                                                                                                                                                                                                                                      97US-0867030.
94US-0243546.
                                                                                                                                                                                                                                                                                                                                      97US-0867030.
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                                                              English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 AA.
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   various enzymatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17;
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                                protein
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RESULT 10
AAY755
XX AAY755
XX 21-MAR
DE Neisse
XW Neisse
XW Neisse
XW Antiba
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CC datermine the serotype of the virus.

CC AR211799, AR211800, AR211801 and AR2118021 may be used in hybridization consumption of the location of DNA flanking serotype-specific cps genes in any strain of S. pneumoniae virus.

CC Additionally, the flanking regions are involved in recombination and integration of the type specific cps genes during virus.

CC and integration of the type specific cps genes during virus construct can be stably integrated of the flanking region, the resulting construct can be stably integrated cof the flanking region, the resulting construct can be stably integrated cof the flanking region, the resulting construct can be stably integrated construct.
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Best Local
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31-JUL-1998;
02-SEP-1998;
02-SEP-1998;
09-CCT-1998;
09-CCT-1998;
09-CCT-1998;
09-CCT-1999;
25-FEB-1999;
                                                                                                                                         Fraser C,
Petergen J
Tettelin H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neisseria meningitidis ORF 747 protein sequence SEQ ID NO:2558.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY75542 standard;
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                                       WPI; 2000-062150/05
N-PSDB; AAZ54304.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY75542;
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                                                                                                                                                                                                                                                                                  (CHIR ) CHIRON CORP.
(GENO-) INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 REIIMD
|:||||
| 52 rkiimd
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5; Conserv
                                                                                                                                             Ä,'n
                                                                                                                                             Galeotti C, Grandi G,
, Pizza M, Rappuoli R,
, Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                        98US-0083758.
98US-0094869.
98US-00998994.
98US-0099062.
98US-0103749.
98US-0103796.
98US-0121528.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-US09346
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                                                                                                                                                                                        Hickey E,
Ratti G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20;
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                                                                                                                                                                                        Masignani V,
Scalato E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 58;
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                                                                                                                                                                                        , Mora M;
Scarselli
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Query Match
Best Local Similarity
Matches 4; Conserv
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31-JUL-1998;
02-SEP-1998;
                                                                                                                                                  09-OCT-1998;
09-OCT-1998;
09-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54577 to AAZ54576 and AAZ54616 to AAZ54573 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
WPI; 2000-062150/05
N-PSDB; AAZ54305.
                                       Fraser C, Galeotti C, Grandi G, Petersen J, Pizza M, Rappuoli R, Tettelin H, Venter JC;
                                                                                                                                                                                                                                                             30-APR-1999;
                                                                                                                                                                                                                                                                                       11-NOV-1999.
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                                                                                                                                                                                                                                                                                                                                          Neisseria meningitidis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY75543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY75543 standard; Protein; 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; Page 1216; 1453pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel Neisserial polypeptides predicted to be useful antigens vaccines and diagnostics \, -
                                                                                                                                                                                            02-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                      antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                       Neisseria meningitidis ORF 747 protein sequence SEQ ID NO:2560
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                                                                                             (CHIR ) CHIRON CORP. (GENO-) INST GENOMIC RES.
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68 reivld 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                   98US-0099062.
98US-0103749.
98US-0103794.
98US-0103796.
99US-0121528.
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98US-0094869.
98US-0098994.
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                                                    Hickey E,
Ratti G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21;
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                                                   Masignani V,
Scalato E,
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                                                      , Mora M;
Scarselli
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Best Local
             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                           Pneumonia;
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유

Novel Neisserial polypeptides predicted

ť

be

useful antigens

Query Match

86.2%;

Score

25; DB 13;

Length

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AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54577 to AAZ54576 and AAZ54616 to AAZ5473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
                                          The amino acid sequence is that 6 which was translated from DNA AAR21409-R21413 and AAR20056.
                                                                                                                                                                                        New DNA sequences which act as oligo:nucleotide assaying DNA sample from respiratory secretion c infected with P carinii
                                                                                                                                         Claim 3; Fig 3; 42pp; English
                                                                                                                                                                                                                                                                                       N-PSDB; AAQ20065.
                                                                                                                                                                                                                                                                                                             WPI; 1992-007487/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NADH dehydrogenase 6.
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68 reivld 73
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4; Conserv
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174 AA;
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                                                                    of P. carinii NADH dehydrogenase from plasmid pAZ112. See also
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                                                                                                                                                                                                              This invention describes novel isolated Streptococcus pneumoniae polynucleotides (see AAZ96173-296494) and their encoded proteins (see CAX96792-Y86182). The DNA, vectors and host cells described in the method of the invention are useful for the recombinant expression of the polypeptides. The polypeptides are useful for treatment or prevention of disease, or diagnosis of disease related to expression or activity of such a polypeptide. They can also be used to screen for compounds which interact with and inhibit or activate such a polypeptide. The polypeptides (or DNA encoding them, via gene therapy) are also useful for inducing an immunological response in a mammal. The antagonists are useful to inhibit such bacterial polypeptides. The polypeptides are cuseful to inhibit such bacterial polypeptides. The polypeptides are cuseful to determine their role in pathogenesis of infection, dysfunction and disease.
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                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 5; Page 551-552; 640pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-159452/14.
N-PSDB; AAZ96394.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stodola RK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Black MT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SMIK ) SMITHKLINE BEECHAM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-AUG-1996;
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antimicrobial; antiblotic; pathogenesis; infection.
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                                                                                                                 Conservative
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1; Mismatches 0;
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2e+02;
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Matches 4
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 WO200006738-A2
                             Streptococcus pneumoniae
                                                       Streptococcus pneumoniae infection; immunogen; antigen; diagnosis; AIDS; bacterial pneumonia; asplenia; heart disease; tung disease; alcoholism; kidney disease; diabetes; fimunosuppressive disorder; otitis media; pneumococcal septicaemia; sinusitis; meningitis; therapy.
                                                                                                                              Streptococcus pneumoniae protein sequence ID119.
                                                                                                                                                             02-JUN-2000
                                                                                                                                                                                         AAY81763;
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a polypeptide of the thymidylate kinase family (tdk polypeptides), and is derived from Ereptococcus pneumoniae. Tdk polypucleotides may be used to recombinantly produce the tdk polypeptides either in vivo (e.g. as part of a genetic vaccination procedure) or in vitro (e.g. as part of a fermentation culture). The nucleic acids and proteins may be used to diagnose diseases in which the tdk polypeptides are expressed, such as infection by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 3; 41pp; English.
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N-PSDB; AAA64398.
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arren PV;
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2e+02;
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This sequence represents a Streptococcus pneumoniae protein of the CC invention. The proteins (or their homologues, derivatives and/or fragments) are useful as immunogens or antigenic compositions comprising the proteins are useful as vaccines and also in diagnostic assays. The sequences are useful for the detection or diagnostic of s. pneumoniae infection, by contacting a sample to be tested with them. Agents capable of antagonising, inhibiting or interfering with the function or expression of the protein or polypeptide are useful in medical compositions in the treatment or prophylaxis of S. pneumoniae infection. As the sequences can be used to treat S. pneumoniae infection, infection. As the sequences can be used to treat bacterial pneumonia, which has high rates in young children, the elderly, and in patients with predisposing conditions young children, the elderly, and in patients with predisposing conditions or with immunosuppressive disporders, especially AIDS. They can also be used to treat pneumococcal septicaemia, otitis media, sinusitis, and
Ouery Match 86.2%; Score 25; DB 21; Length 212; Best Local Similarity 66.7%; Pred. No. 2è+02; Matches 4; Conservative 2; Mismatches 0; Indels
                                                                                                     Sequence
                                                                                                                                           meningitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Page 61; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcal proteins and polynucleotides useful for diagnosis, treatment and prophylaxis of bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-195301/17.
N-PSDB; AAZ91859.
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19-MAR-1999;
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99US-0125329.
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Search completed: March 18, 2002, 09:48:56 Job time: 365 sec

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   US-09-544-665-4
29
1 REIIMD 6
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Gapop 10.0 , Gapext 0.5
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep: *
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/cgn2_6/ptodata/2/iaa/6B_COMB.pep: *
/cgn2_6/ptodata/2/iaa/backfiles1.pep: *
/cgn2_6/ptodata/2/iaa/backfiles1.pep: *
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US-08-667-0330-7
PCT-USS-06119-7
US-09-259-109-2
US-08-781-020-6
US-09-388-65-386-23
US-08-840-204-3
US-08-840-204-3
US-08-181-318-3
US-08-181-318-3
US-08-181-318-6
US-08-477-1108A-6
US-08-477-1108A-6
US-08-477-112-6
PCT-US-99-08-322-6
US-08-315-461-7
US-08-315-461-7
US-08-381-817A-4
US-08-481-700B-8
US-09-026-408-3
US-08-481-700B-8
US-09-026-408-3
US-08-325-547-4
US-08-325-547-3
US-08-325-547-3
US-08-426-627-20
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US-08-867-030B-7
US-08-867-030B-7
Sequence 7, Application US/08867030B
Patent No. 5948900
GENERAL INFORMATION:
APPLICANT: Yother et al.
TITLE OF INVENTION: Streptococcus pneumoniae
TITLE OF INVENTION: Capsular Polysaccharide Genes and
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/370,253
CURRENT FILING DATE: 1999-08-09
EARLIER APPLICATION NUMBER: 60/097,222
EARLIER FILING DATE: August 20, 1998
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Microsoft Office 97
SEQ ID NO 4
LENGTH: 259
TYPE: PRT
ORGANISM: Zea mays
US-09-370-253-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-370-253-4
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Matches 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Allen, Stephen M.
APPLICANT: Sakai, Hajime
APPLICANT: Thorpe, Catherine J.
TITLE OF INVENTION: Amino Acid Transporters
FILE REFERENCE: BB-1200
                             ADDAGE STREET: BULL STREET: BULL STATE: TX
STATE: TX
USA
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STATE: TX
COUNTRY: USA
ZIP: 77071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch floppy
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246 RQIIMD 251
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nes 5; Conservative
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E: Benjamin Aaron Adler,
8011 Candle Lane
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US-08-766-738-3

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US-08-578-709-13

US-08-560-098A-55

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US-08-336-031-2

US-08-396-035-67

US-08-902-853-7

PCT-US95-06725-2

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US-08-968-4760A-67

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Result No.

Minimum Maximum

Gaps

0

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; ORIGINAL SOURCE:
; IMMEDIATE SOURCE:
; POSITION IN GENOME:
US-08-867-030B-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCT-US95-06119-7
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
COMPUTER: TEM PC COMPATION
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOSTWARE: #1.30
SOSTWARE: #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06119
FILING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/243,546 FILING DATE: May 16, 1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867,030B
FILING DATE: June 2, 1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/243,546
APPLICATION NUMBER: 08/243,546
                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/243,546
FILING DATE: 16-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: D5
FELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 777-2321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 REIIMD 6
|:||||
52 RKIIMD 57
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                   TTLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YPOTHETICAL: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Benjamin Aaron Adler, Ph.D., J.D. REGISTRATION NUMBER: 35,423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                         COUNTRY: U
                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DESCRIPTION: protein
                                                                                                                                                                                                                                                                                                  NDDRESSEE: Arnold, White & Durkee
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                                                                                                                                                                                                                                                                                    Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                               Application PC/TUS9506119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                      United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Microsoft Word for Macintosh
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Pred. No.
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    Mismatches

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17;
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                                                                                                                                                                                                                                                                                                                                                                                      ; LENGTH: 212
TYPE: PRT
; ORGANIZM: Streptococcus pneumoniae
US-09-259-109-2
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US-09-259-109-2
                                                                                                                                                                              RESULT 5
US-08-781-020-6
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 2
                                                                                                                                  Sequence 6, Applicati
Patent No. 5792749
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/259,109
CURRENT FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ingraham, Karen A.
APPLICANT: Traini, Christopher M.
APPLICANT: Warren, Patrick V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Burnham, Martin K. R.
APPLICANT: Zalacain, Magdalena
APPLICANT: Biswas, Sanjoy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (512) 418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: 1. MOLECULE TYPE:
     CORRESPONDENCE ADDRESS:
ADDRESSEE: WHITHAM, CURTIS, WHITHAM & MCGINN
STREET: Reston Intl. Center, 11800 Sunrise Valley Dr.,
STREET: Suite 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 REIIMD 6
|:|||
52 RKIIMD 57
                                                                                  TITLE OF INVENTION:
                                                                     UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                             51 REVILD 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER:
                                                                                                                                                                                                                                                           1 REIIMD 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Parker, David L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FastSEQ for Windows Version 3.0
                                                                                                                                                                Application US/08781020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/09259109
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linear
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                                                                                  H. Tonie
METHOD AND COMPOSITION FOR LOWERING LOW
DENSITY LIPOPROTEIN CHOLESTEROL
                                                                                                                                                                                                                                                                                                                        86.2%;
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Pred. No.
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Pred No. 67;
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0; Gaps

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

COUNTRY:

USA

20191

Reston : VA

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Query Match
Best Local Similarity
Watches 5; Conserva
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RESULT .7
US-08-565-386-23
                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-09-038-935-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 82.8%; Score 24; Best Local Similarity 100.0%; Pred. No. Matches 5; Conservative 0; Mismatc
                                                                                                                                                                                                                                                                       SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence 6, Application US/09038935
Patent No. 6150332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/038,935
CURRENT FILING DATE: 1998-03-12
EARLIER APPLICATION NUMBER: 08/781,020
EARLIER FILING DATE: 1997-01-19
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wright, H. Tonie
APPLICANT: Janciauskiene, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                      ITLE OF INVENTION: METHOD AND COMPOSITION FOR LOWERING LOW DENSITY ITLE OF INVENTION: LIPOPROTEIN CHOLESTEROL
LE REFERRNCE: 290222ba
"RRENT APPLITAMTON"
                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: VC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-391-2510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 EIIMD 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Whitham, Michael E.
REGISTRATION NUMBER: 32,635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 EIIMD 6
                                                                                2 EIIMD 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                              5 EIIMD 9
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                                                                                                                                                                                                                                                                                       PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 amino acids
                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-JAN-1997
                                                                                                                                         82.8%; Score 24; DB 4; Length 33; 100.0%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US/08/781,020
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                                                                                                                            Mismatches
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                                                                                                                            0; Indels
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                                                                                                                            Gaps
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LENGTH: 96 amino acids
TYPE: amino acid
STRANDEDNESS: not releva
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-565-386-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-403-866-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/08403866 Patent No. 5643779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 23, Application US/08565386 Patent No. 5741697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                  APPLICANT: Renault, Pierre
TITLE OF INVENTION: Nucleic
TITLE OF INVENTION: Synthase
NUMBER OF SEQUENCES: 16
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: BACTERIOPHAGE OF CHLAMYDIA PSITTACI NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
NAME: GOLDMAN, MICHAEL L.
REGISTRATION NUMBER: 30, 727
REFERENCE/DOCKET NUMBER: 207
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1600
TELEFAX: (716) 263-1487
                                                                                                    FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 96 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 716-263-1636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Bavoil, Patr
APPLICANT: Hsia, Ru-chi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35 RDVVMD 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 176/60040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/565,386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 REIIMD 6
                                                                                                                                                                                    APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                               Godon, Jean-Jacques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        716-263-1600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               not relevant
                                                                                                                                                                                                                                                                                                                                                    Nucleic acid coding for an alpha-acetolactate synthase from Lactococcus and its application
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                                                                                                                                                                                      US/08/403,866
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                                                             20747/30
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Best Local Similarity 83.3
"There's 5; Conservative
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tent No. 6103498
                                                                                                                                                                                                                 NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LIVNAT, SHMUEL
REGISTRATION NUMBER: 33,949
REFERENCE/DOCKET NUMBER: 30,949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162 REIAMD 167
351 EIIMD 355
                                                                                                                                                                                                                                                                                              ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 978450 (WUT)
ORMATION FOR SEQ ID NO:
                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: si
                                                          Local Similarity es 5; Conserv
                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 REIIMD 6
                             2 EIIMD 6
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/840,204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM:
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ECULE TYPE: PIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RGANISM: Lactococcus lactis subsp. lactis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LICANT: STEFANSSON, STEINGRINDR P.
E OF INVENTION: MUTANT PLASNINGEN ACTIVATOR-INHIBITOR
E OF INVENTION: TYPE 1 (PAI-1) AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UENCE CHARACTERISTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ER OF SEQUENCES:
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                                                                                                                                                                                                379 amino acids
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                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAWRENCE, DANIEL A.
                                                                                                                                                      linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MORRISON & FOERSER
                                                                                                                                                                                                                                                                              (202) 887-1500
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                                                                          82.8%;
                                                                                                                                                                                                                                                                                                           30807-20004.00
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Pred. No. 1.9e+02;
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                                                                                        Length 379;
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                                                          Indels
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US-08-650-275-3
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                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local 9
                                                                                                                                                                                                   Sequence 3, Application US/09181318 Patent No. 6001632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, A
Patent No. 57
                                                                                                                                                                                                                                09-181-318-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                      ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: GI 1086627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/650,275 FILING DATE: Filed Herewith ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                        313 REFVMD 318
                                                                                                                                                                                                                                                                                                                                               Local Similarity 66.
                                                                     CITY: Palo Alto
                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: UZIP: 94304
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                                         COUNTRY:
                                                                                                                               TLE OF INVENTION: HUMAN PROTEIN DISULFIDE ISOMERASE MBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                    1 REIIMD 6
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LECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER:
                                                                                                  ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELEPHONE:
                              94304
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                                                                                  3174 Porter Drive
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                                         U.S.
                                                                                                                                                       Murry, Lynn
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                                                                                                                                                                       Braxton, Scott Michael
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                                                                                  Incyte Pharmaceuticals, Inc.
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                                                                                                                                                                                                                                                                                                                                                               Score 24;
Pred. No.
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Query Match 82.
Best Local Similarity 66.
Matches 4; Conservative
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                FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/
FILING DATE: 09/01/97
APPLICATION NUMBER: 07/
APPLICATION NUMBER: 07/
APPLICATION NUMBER: 07/28/92
APPLICATION NUMBER: 07/
FILING DATE: 02/28/91
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                                                                                                                                                                                                 COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordberfect (Version 5.1)
CURRENT APPLICATION DATA:
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LENGTH: 389 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: GI 1086627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/650,275
FILING DATE: 02/28/91 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Di
                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   313 REFVMD 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Luther, Barbara J. REGISTRATION NUMBER: 33,954 REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                             STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                    CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/181,318
                                                                                                                                                                                   APPLICATION NUMBER: US/08/121,714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             LE OF INVENTION: MASPIN, A NOVEL SERPIN WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION:
CANT: Sager, Ruth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            415-852-0195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                415-855-0555
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                                                                                                           07/938,823
                                   07/662,216
                                                                      07/844,296
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Pred. No. 2.2e+0
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Query Match
Best Local Similarity luv.
Thes 5; Conservative
                                                                                                                                                                                                          APPLICATION NUMBER: 07/93
FILING DATE: 09/01/92
APPLICATION NUMBER: 07/844
FILING DATE: 02/28/92
APPLICATION NUMBER: 07/662
APPLICATION NUMBER: 07/662
APPLICATION NUMBER: 07/662
APPLICATION INFORMATION:
NAME: Fraser, Jante V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -08-477-108A-6
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                                                                    TELEFAX: (617) 542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,108A
FILLING DATE: June 7, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06
FILING DATE: 09/01/93
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RELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             374 EIIMD 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ITLE OF INVENTION: MASPIN, A NOVEL SERPIN WITH ITLE OF INVENTION: TUMOR SUPPRESSING ACTIVITY
                                                                                                                               REFERENCE/DOCKET NUMBER: 06570/002002
TECONMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: MS-DOS (Version 5 SOFTWARE: WordPerfect (Version 5.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
STRANDEDNESS:
TOPOLOGY: linear
                                                   LENGTH:
                                                                                                                                                                                              NAME: Fraser, Janis K
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 EIIMD 6
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                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          225 Franklin Street
                                                                                                                         (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anisowicz,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sager, Ruth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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PCT-US93-08322-6

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; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-477-112-6
RESULT
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                                                                                                                                                                                                     Query Match
Best Local Similarity
Watches 5; Conserv:
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US-08-477-112-6
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PRIOR APPLICATION DATA:
APPLICATION UNBER: 08/121;714
FILING DATE: 09/01/93
APPLICATION NUMBER: 07/938,823
FILING DATE: 09/01/92
APPLICATION NUMBER: 07/844,296
FILING DATE: 02/28/92
APPLICATION NUMBER: 07/662,216
APPLICATION UNBER: 07/662,216
APPLICATION UNBER: 07/662,216
APPLICATION TIMESTER O7/662,216
APPLICATION TIMESTER O7/662,216
APPLICATION TIMESTER O7/662,216
APPLICATION TIMESTER OF T
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SEQUENCE CHARACTERISTICS:
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tent No. 5905023
ENERAL INFORMATION:
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OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WOODPERECT (Version 5.1)
CURRENT APPLICATION MINE.
APPLICATION MINE.
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MEDIUM TYPE: 3.5* D1
                                                                                            374 EIIMD 378
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les 5; Conserv
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REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 06
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APPLICATION NUMBER: 07/938

FILING DATE: 09/01/92

APPLICATION NUMBER: 07/844

FILING DATE: 02/28/92

APPLICATION NUMBER: 07/662

APPLICATION NUMBER: 07/662

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APPLICATION NUMBER: 07/662

APPLICATION NUMBER: 07/662
                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
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                                                                                374 EIIMD 378
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REGISTRATION NUMBER: (
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                                                                                                                                               Conservative
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                                                                                                                                                                                                                                              linear
                                                                                                                                             82.8%; Score 24; DB 5; 1
100.0%; Pred. NO. 2.2e+02
Live 0; Mismatches 0
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C;Species: Methanococcus jannaschii
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### ALIGNMENTS

C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jul-2000
C;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jul-2000
C;Accession: C64364
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Black, Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, Reich, C.I.; Sadow, P.M.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woes, A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woes, A;Atcession: C64364
A;Accession: C64364
A;Accession: C64364 hypothetical protein C17E7.8 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 \*sequence\_revision 29-Oct-1999 \*tc.Accession: 731823 C;Accession: 731823 R;Bradshaw, H. A;Experimental source: strain Bristol N2; C;Genetics: A;Gene: CESP:C17E7.8 A;Map position: 5 A;Introns: 27/3; 64/1; 164/3; 242/3; 326/1 submitted to the EMBL Data Library, July 1997
A;Description: The sequence of C. elegans cosmid C17E7
A;Reference number: Z21091
A;Accession: T31823 A;Map position: REV458767-457625 C;Superfamily: NADH dehydrogenase (ubiquinone) 49K protein A; Status: preliminary; translated A; Molecule type: DNA A; Residues: 1-413 - GRRA> A; Cross-references: EMBL: AF016443; A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type; DNA A;Residues: 1-380 <BUL> A;Cross-references: GB:U67501; GB:L77117; NID:g2826289; EMBL:AF016443; PIDN:AAC24282.1; GSPDB:GN00023; CESP:C17E7.8 se: strain Bristol N2; clone C17E7 #sequence\_revision 29-Oct-1999 #text\_change 100.0%; 0; Score 29; Pred. No. from GB/EMBL/DDBJ Mismatches 16; 2; 0; Length 380; Indels PIDN: AAB98504.1; PID:g15912: 29-Oct-1999 0 Gaps 0

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C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 31-Mar-2001
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RESULT
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Jenome Res. in press, 2001
N:Title: The complete genome
A:Reference number: A86625
A:Reference F86742
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Date: 08-May-1998 #sequence_revision 08-May-1998; Accession: B70482
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cross-references: GB:AE000774; NID:g2984324; PIDN:AAC07846.1; Experimental source: strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. Reference number: A70300; MUID:98196666 Accession: B70482 Status: preliminary; nucleic acid sequence not shown; translation not shown Molocule transcrive.
                                                                                                                                                                                   ;Superfamily: virulence-associated protein vacB homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Molecule type: DNA
Residues: 1-456 <AQF>
                                                                                                        Matches
                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                               Molecule type: DNA
Residues: 1-817 <STO>
Cross-references: GB:AB005176; NID:g12723878;
Experimental source: strain II1403
                                                                                                                                                                                                                                                                                                                                                                                        Accession: F86742
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371 REVIMD 376
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290 REIIMD 295
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                                             4 REVIMD 9
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                                                                                                      Score 28;
Pred. No.
1; Mismatc
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Pred. No.
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                                                                                                                          DB 2;
69;
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                                                                                                                                                                                                                                                  PIDN: AAK05040.1;
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Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, kl. S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reev J. Bacteriol, 179, 7135-7155, 1997
A.Title: Complete genome sequence of Mothers Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ş
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A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R:Kawarabayasi, Y.; Sawada, M.;
M.; Ohfuku, Y.; Funahashi, T.;
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein PH1943 - C;Species: Pyrococcus horikosh C;Date: 14-Aug-1998 #sequence_C;Accession: G71209
                                                                                                 conserved hypothetical protein MTH545 - Methanobacterium thermoautotrophicum C;Species: Methanobacterium, thermoautotrophicum C;Darcie: 05-Dec-1997 *sequence_revision Cpace: 1997 *text_change 22-Oct-1999 C;Accession: A69172 te-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Ald R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Ald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-340 <TON>
A;Cross-references: GB:AE000647; GB:AE000511; NID:92314645; PIDN:AAD08509.1; PID:923
C;Superfamily: branched-chain-amino-acid transaminase BAT1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; A;Title: The complete genome sequence of the gastric pathogen Hel A;Reference number: A64520; MUID:97394467 A;Recession: D64703
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C;Superfamily: Methanococcus conserved hypothetical protein MJ1638
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A; Residues: 1-243 <KAW>
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A69172
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son, J.D.; Kelley, J.M.
Nature 388, 539-547, 19
A; Authors: Wallin, E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: D64703
R; Tomb, J.F.; White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 29-Sep-1999
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Best Local S
Matches 5
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Best Local Similarity
Matches 5; Conserv
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270 REILMD 27
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5; Conserv
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genome sequence of Methanobacterium thermoautotrophicum Delta r\colon A69000;\ MUID:98037514
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Tanaka, T.; Kudoh, Y.; Yame
                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 46;
1; Mismatches
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32;
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Yamazaki, J.;
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                                                                                          J.; Aldredge,
son, R.; Jiwani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fleischmann,
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Watthey
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hypothetical protein YPL004c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein LPAl3c; hypothetical protein YP8132.09c
c;Species: Saccharomyces cerevisiae
C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 12-Dec-1997
C;Accession: S52527; S59689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: B71661
R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, Nature 396, 133-140, 1998
A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria. A;Reference number: A71630; MUID:99039499
A;Accession: B71661
A;Status: preliminary: nucleic acid sequence not shown; translation not shown
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C;Species: Rickettsia prowazekii
C;Date: 21-Nov-1998 *sequence_revision 21-Nov-1998 *text_change 03-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AJ235272; GB:AJ235269; NID:g3861033; PIDN:CAA15012.1; PID:e134285
A;Experimental source: strain Madrid E
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A; Residues: 1-341 <HAL>
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Best Local Similarity 83.:
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Experimental source: strain AB972; Baperimental source: strain AB972; Ball, J.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Storms, R.K.; Vo, D.H.; Walbalt ted to the EMBL Data Library, August 1995; Description: The sequence of Saccharomyces cerevisiae chromosome XVI left arm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molecule type: DNA
Residues: 1-327 <AI
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Reference number: S52519
Accession: S52527
Molecule type: DNA
Residues: 1-341 <BAD>
Cross-references: EMBL:248483; NID:9683777; PID:9683786; MIPS:YPL004c
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Best Local Similarity
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83.3%;
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Pred. No.
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Pred. No.

    Mismatches

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320 REIILD 325

search completed: March 18, 2002,
Job time: 241 sec

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C;Accession: T41879

R;Gomi, S.; Majima, K.; Maeda, S.

J; Gen. Virol. 80, 1323-1337, 1999

A;Title: Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus.

A;Reference number: Z22020; MUID:99281911

A;Accession: T41879

A;Residus: preliminary; translated from GB/EMBL/DDBJ

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-476 KRAM

A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACMNPV orf142 - Bombyx mori nuclear polyhedrosis virus (isolate T3) C;Species: Bombyx mori nuclear polyhedrosis virus, BmSNPV A;Variety: isolate T3 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-384 <STO>
A;Cross-references: GB:AP000398; GSPDB:GN00144
                           Ş
                                                                                                                                                                                                                                                                                                                        A;Note: Orf_118
C;Superfamily: Orgyla pseudotsugata nuclear polyhedrosis virus hypothetical protein 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: fts2; BU212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Title: Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 407, 81-86, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:L33180; NID:g3745835; PIDN:AAC63808.1; PID:g3745961
A;Experimental source: isolate T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity bb..
Conservative
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                                                                                                         Query Match
Best Local Similarity
Matches 5; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                           Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genetics:
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1 REIIMD 6
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                                                                                                                       Conservative
                                                                                                                                                                89.7%;
83.3%;
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                                                                                                                                                                Score 26; DB 2;
Pred. No. 1.2e+0;
                                                                                                                            Mismatches
                                                                                                                                                                .2e+02
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type; DNA A;Residues: 1-437 kMTH. A;Residues: 1-437 kMTH. A;Cross-references: GB;AE000837; GB:AE000666; NID:g2621613; PIDN:AAB85051.1; PID:g262167 A;Cross-referencal source: strain Deita H C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Map position: 1
C;Superfamily: glucose-6-phosphate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: MTH545
                                                                                                                                                                                                                                  DNA polymerase III, epsilon chain (dnaQ) RP732 - Rickettsia prowazekii C;Species: Rickettsia prowazekii C;Species: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000 C;Accession: A71633 Comorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T Rickett 396, 133-140, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lucose-6-phosphate 1-dehydrogenase - Deinococcus radiodurans (strain
;Species: Deinococcus radiodurans
;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .Cross-references: GB:AE002003; GB:AE000513; NID:g6459358; PIDN:AAF11158.1; PID:g645936; Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Accession: B75377
White, O.; Elsen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, M.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 93.:
Best Local Similarity 66.:
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 93...
Best Local Similarity 83...
Matches 5; Conservative
                                                                                                                                                                          Title: The genome sequence of Rickettsia Reference number: A71630; MUID:99039499 Accession: A71633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Status: preliminary
Molecule type: DNA
Residues: 1-590 <WHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lence 286, 1571-1577, 1999
Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans Reference number: A75250; MUID:20036896
Accession: B75377
                                                                                                                                                        Status: preliminary; nucleic acid sequence
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                                                                                                                  type: DNA
: 1-229 <AND>
19
                                                                              nces: GB:AJ235273; GB:AJ235269; NID:g3861237; PIDN:CAA15161.1;
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83.3%;
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                                                                                                                                                        shown;
                                                                                                                                                                                                                                                          J.O.; Sicheritz-Ponten, T.; Alsmark,
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C;Accession: A71681
R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmarl Nature 366, 133-140, 1998
A;Tille: The genome sequence of Rickettsia prowazekii and the origin of mitochondria A;Reference number: A71630; MUID:99039499
                                                                                                                                                                                                                                                                                                                                                                                                                                                            pyruvate dehydrogenase El component, alpha chain precursor (pdhA) RP261 - Rickettsia C;Species: Rickettsia prowazekii C;Bate: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein
A; Residues: 1-64,'X',66,'X',68-69 <MO2>
C; Superfamily: band 3 anion transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R:Moriyama, R.; Makino, S.
Arch. Blochem. Blophys. 256, 606-617, 1987
A;Title: Interaction of glyceraldehyde-3-phosphate dehydrogenase f band 3 polypeptide.
A;Reference number: A61591; MUID:87297550
A;Accession: A61591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    band 3 anion transport protein - bovine (fragments) C;Species: Bos primigenius taurus (cattle) C;Date: 21-Nov-1993 #sequence_revision 28-Apr-1995 C;Accession: S05658; A61591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
S05658
                                                                                                                                                               C; Superfamily: pyruvate dehydrogenase (lipoamide) alpha chain; thiamin pyrophosphate
                                                                                                                                                                                                                          A;Cross-references: GB:AJ235271; GB:AJ235269;
A;Experimental source: strain Madrid E
                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-326 <AND>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Moriyama, R.; Kawamatsu, S.; Kondo, Y.; Tomida, M.; Makino, S. Arch. Biochem. Biophys. 274, 130-137, 1999
A.Title: Antigenic determinants of the cytoplasmic domain of band 3 from bovine eryt. A.Title: Antigenic S05658; MUID:89372925
                                                                                                                                                                                                                                                                                          A.Accession: A71681
A.Accession: A71681
A.Status: preliminary; nucleic acid sequence not shown; translation not shown
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Best Local
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Best Local Similarity 83.3
Matches 5; Conservative
                                                           Matches
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Best Local
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1 REIIMD 6
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5; Conserv
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4; Conservative
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66.78;
                                                                              89.7%;
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Pred. No. 53;
1; Mismatches
                                                           Score 26; DB Pred. No. 79; 1; Mismatches
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                                                                                                                                                                                                                                                  NID: g3868717;
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277 REIILD

OM protein - protein search, using sw model GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

Title: Perfect score: Sequence: US-09-544-665-4 29

Run on:

March 18, 2002, 09:52:26; Search time 24.53 Seconds (without alignments) 8.968 Million cell updates/sec

Scoring table: 1 REIIMD 6

BLOSUM62 Gapop 10.0 , Gapext 0.5 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters:

100059

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

115 115 115 116 117 117 117 117 117 117 117 117 117	100 100 100 100 100 100 100 100 100 100	Result
	0 N N N N N N N N N N N N N N N N N N N	Score
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	~~~~~~~~~~~~~~~~~ <u></u>	% Query Match
578 728 728 728 728 1986 120 123 1123 1155 1175 200 200 200 200 200 200 200 300 300 303 313 313	440 340 322 324 404 404 404 404 404 404 404 404 404 4	Length
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EFZ-HALHA ASHI_SCHPO BAII_HUMAN WALEMENI VILK_BPCHP CYSS_YEAST CSSA_MOUSE RLI3_ARCFU GRPE_ECOLI KTHY_DEIRA FPG_ZYMO SESTRY NARE_CHICK P2A_BRANA PO_STRY NARE_CHICK P2A_BRANA PO_STRY NARE_CHICK P2A_BRANA PAA_BRANA PAA_BRANA PAA_BRANA PAA_BRANA PAA_ARATH P2AA_MEDSA	HEMN_AQUAE TILVE_HELPY TIG_NEUCR DP3E_RICPR ODDA_RICPR ODDA_RICPR ODDA_RICPR V142_NPVAC NITU_BACSU PSAF_HORNU THIL_PYRHO	ID
199217 nomo sapien p18023 halobacteri o13921 schizosacch o13921 schizosacch o13921 schizosacch o13921 schizosacch o13921 schizosacch o13921 schizosacch o13921 secheriopha p40312 saccharomyc o55186 mus mussculu o29450 aeropyrum p o28367 archaeoglob p09372 scherichia o9xy40 deinococcus o9xy40 deinococcus o9xy40 deinococcus o9xy40 zymomonas m o58890 methanococc o11109 streptomyce o92080 gallus gall p23778 brassica na p071100 arabidopsis p48578 arabidopsis p48578 arabidopsis		5

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1 REIIMD 6 ||:||| 371 REVIMD 376

Ouery Match 96.6%; Score 28; DB 1; Length 456; Best Local Similarity 83.3%; Pred. No. 19; Matches 5; Conservative 1; Mismatches 0; Indels

0;

Gaps

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RESULT

45	44	43	42	41	4.0	39	38	37	36	35	34
24	24	24	24	24	24	24	24	24	24	24	24
82.8	82.8	82.8	82.8	82.8	82.8	82.8	82.8	82.8	82.8	82.8	82.8
531	499	493	444	402	402	402	400	384	372	340	337
-ب	μ	<u>س</u>		μ.	1	<b>ب</b> سو	_	μ	ы		<u>, , , , , , , , , , , , , , , , , , , </u>
TCPY_MOUSE	C771_SOLME	YDAK_CAEEL	P44_PANTR	PAI1_PIG	PAI1_HUMAN	PAI1_BOVIN	PAI1_MUSVI	FTSZ_BUCAP	3BHS_BOVIN	ILVC_LACLA	2265_HUMAN
Q61390 mi	P37123 Sc	P90771 ca	P27473 pa	P79335 SI	P05121 h	P13909 bo	P50449 mu	051929 bi	P14893 b	Q02138 1a	095218 hc
us musculu	olanum mel	aenorhabdi	an troglod	us scrofa	omo sapien	os taurus	mustela vis	uchnera ap	3 beta-hy	actococcus	omo sapien

# ALIGNMENTS

us-09-544-665-4.rsp

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RESULT 3
TBG_NEUCR
ID TBG_N
AC P5337
DT 01-OC
DT 01-OC
DT 20-AU
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                                                                                                                                                                                              Query Ma
Best Loc
Matches
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15-JUL-1998 (Rel. 36,
20-AUG-2001 (Rel. 40,
BRANCHED-CHAIN AMINO A
ILVE OR HP1468.
TBG_NEUCR
P53377;
01-OCT-1996
01-OCT-1996
20-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TLVE_HELPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-26695 / AfCC 700392;
MEDLINE-97394467; PubMed-9252185;
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.
Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
MCKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.
Cotton M.D., Weldman J.M., Fujil C., Bowman C., Watthey L., Wallin
Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
Venter J.C.;
                                                                                                                                                                                                                                                                                        Pyridoxal
BINDING
                                                                                                                                                                                                                                                                                                              Pfam; PF01063; aminotran_4; 1.
ProDom; PD001961; Aminotran_4; 1.
PROSITE; PS00770; AA_TRANSFER CLASS_4; 1.
Transferase; Aminotransferase; Branched-chain amino acid biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE000647; AAD08509.1; -. HSSP; P00510; 1A3G. TIGR; HP1468; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pylori.";
Nature 388.539-547(1997),
CATALYTIC ACTIVITY: L-LEUCINE + 2-OXOGLUTARATE - 4-METHYL-2-
OXOPENTANOATE + L-GLUTAMATE (ALSO ACTS ON L-ISOLEUCINE AND
                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        026004;
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                                                                                                                                       270
                                                                                                                                                                                                                                                                                                                                                                                [nterPro;
                                                                                                                                                                                                            y Match
Local
                                                                                                                                                        1 REIIMD 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COFACTOR: PYRIDOXAL PHOSPHATE.
PATHWAY: VALINE AND ISOLEUCINE BIOSYNTHESIS.
SIMILARITY: BELONGS TO CLASS-IV OF PYRIDOXAL-PHOSPHATE-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMINOTRANSFERASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complete genome sequence of
                                                                                                                                       REILMD
                                                                                                                                                                                              Similarity 83...
5; Conservative
                                                                                                                                                                                                                                                                     phosphate; Complete proteome.

187 187 PYRIDOXAL PHOSPHATE (BY SIMILARITY).

340 AA; 37641 MW; 84F1685F61DC5C2C CRC64;
                                                                                                                                                                                                                                                                                                                                                                            IPR001544; Aminotran_4.
 (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                       275
                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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. 36, Last sequence 40, Last annotation
                                                                                                                                                                                                            93.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               epsilon subdivision; Helicobacter group;
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                                                                                                                                                                                             Score 27; DB
Pred. No. 24;
1; Mismatches
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Matches 4
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SEQUENCE
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Neurospora crassa.

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Sordariales; Sordariaceae; Neurospora.

NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DP3E_RICPR STANDARD; PRT; 2
OP3CJ9;
O92CJ9;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence up
30-MAY-2001 (Rel. 40, Last annotation
DNA POLYMERASE III, EPSILON CHAIN (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE-98019102; PubMed-9358070;

Heckmann S., Schliwa M., Kube-Granderath E.;

Heckmann S., Schliwa M., Kube-Granderath E.;

"Primary structure of Neurospora crassa gamma-tubulin.";

"Primary structure of Neurospora crassa gamma-tubulin.";

Gene 199:303-309(1997).

1. FUNCTION: TUBULIN IS THE MAJOR CONSTITUENT OF MICROTUBULES.

GAMMA TUBULIN IS FOUND AT MICROTUBULE ORGANIZING CENTERS (NTOC.)

SUCH AS THE SPINDLE POLES OR THE CENTROSOME, SUGGESTING THAT IT IS INVOLVED IN THE MINUS-END NUCLEATION OF MICROTUBULE ASSEMBLY.

1. SIMILARITY: BELONGS TO THE TUBULIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                   Rickettsia prowazekii.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiacae; Rickettsieae; Rickettsia.
NCBI_TaxID=782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000217; Tubulin.
InterPro; IPR003008; Tubulin_Fts2.
Pfam; PF00091; tubulin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNAQ OR RP732.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X97753; CAA66348.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Microtubules;
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PRO1164; GAMMATUBULIN.
; PS00227; TUBULIN; 1.
bules; GTP-binding.
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; 70D0CBEA224B6343 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    update): 2.7.7.7).
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                                 BACTERIA.
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Best Local
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                               NATURE 396:133-140(1998).

-IT FUNCTION: THE PYRUVATE DEHYDROGENASE COMPLEX CATALYZES THE OVERALL CONVERSION OF PYRUVATE TO ACETYL-COA & CO(2). IT CONTAINS MULTIPLE COPIES OF THREE ENZYMATIC COMPONENTS: PYRUVATE DEHYDROGENASE (E1), DIHYDROLIPOANIDE ACETYLTRANSFERASE (E2) & LIPOANIDE DEHYDROGENASE (E3) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                MEDLINE-9903949; PubMed-9823893;
Andersson S.G.E., Zomorodipour A., Andersson J.O.,
Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund Eriksson A.-S., Winkler H.H., Kurland C.G.;
The genome sequence of Rickettsia prowazekii and the origin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; alpha subdivision; Rickettsiales; Rickettsiaceae; Rickettsieae; Rickettsia. NCBI_TaxID=782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence up
30-MAG-2010 (Rel. 40, Last annotation
PYROVATE DEHYDROGENASE E1 COMPONENT, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RICPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00929; Exonuclease; 1.
SMART; SM00479; EXOIII; 1.
Transferase; DNA-directed DNA polymerase; DNA replication; Exonuclease; Complete proteome.
SEQUENCE 229 AA; 26078 MW; CA7ADE72E6E38D90 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-MADRID E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rickettsia prowazekii.
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                                                                                                                                                                                                                                                                                                                                   mitochondria."
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nes 5; Conserv
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N PYROPHOSPHATE + DNA(N).
N PYROPHOSPHATE + DNA(N).
SUBBUNIT: COMPAINS A CORE (COMPOSED OF ALPHA, EPSILON, AND THETA SUBBUNIT HAT ASSOCIATES WITH A TAU SUBUNIT WHICH ALLOW THE CORE DIMERIZATION TO FORM THE POLITI COMPLEX. POLITI ASSOCIATES WITH THE GAMMA COMPLEX (COMPOSED OF CHAINS GAMMA, DELTA, DELTA', PSI, AND CHI) AND WITH THE BETA CHAIN (BY SIMILARITY).
                                                                                                                     CATALYTIC ACTIVITY: PYRUVATE + LIPOAMIDE = S-ACETYL-DIHYDRO-
LIPOAMIDE + CO(2).
COFACTOR: THIAMINE PYROPHOSPHATE (BY SIMILARITY).
SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | REIIMD 6
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Pred. No.
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MBL outstation -
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Query Match Best Local S Matches 4

Similarity 66. 4; Conservative

89.7%;

Score 26; Pred. No.

. 49;

Length 384

Mismatches

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Best Local
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20-AUG-2001 (Ru
20-AUG-2001 (Ru
20-AUG-2001 (Ru
CELL DIVISION )
FTSZ OR BU212.
                     INTERPRO I IPRO00158; FtsZ.
InterPro; IPRO00158; Ttbulin_FtsZ.
InterPro; IPRO003008; Tubulin_FtsZ.
InterPro; IPRO03108; Tubulin; 1
PROSITE; PS01134; FTSZ_1; 1
PROSITE; PS01134; FTSZ_2; 1
PROSITE; PS01135; FTSZ_2; 1
PROSITE; PS01135; FTSZ_2; 1
PROSITE; PS01135; TTSZ_1; TTSZ_
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDILINE-20445173; PubMed-10993077;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
"Genome sequence of the endocellular bacterial symbiont of aphids
Buchnera sp. APS.";
Nature 407:81-86 (2000).

1- FUNCTION: THIS PROTEIN IS ESSENTIAL TO THE CELL-DIVISION PROCESS.

1- FUNCTION: THIS PROTEIN IS ESSENTIAL TO THE CELL-DIVISION WILL OCCUR,
THE CYTOPLASMIC MEMBRANE AT THE PLACE WHERE DIVISION WILL OCCUR,
AND THE FORMATION OF THE RING IS THE SIGNAL FOR SEPTATION TO
BEGIN. BINDS TO AND HYDROLYZES GTP (BY SIMILARITY).

1- SUBBURIT: AGGREGATE TO FORM A RING-LIKE STRUCTURE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AJ235271; CAA14723.1; -.
InterPro; IPRO01017; E1_dh.
Pfam; PR00576; E1_dehydrog; 1.
Glycolysis; Oxidoreductase; Flavoprotein; Thiamine pyrophosphate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
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P57308;
                                                                                                                                                                                                                                                                                                                     EMBL; AP001118; BAB12929.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Buchnera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  symbiotic bacterium)
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5; Conserv
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(Rel. 40,
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    Α̈́,
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             41308
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Last sequence update)
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FTS2.
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Pred. No.
             477023ECBEC44792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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             CRC64;
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RESULT 8
              REPRESENTATION OF THE PROPERTY OF THE PROPERTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 89. Best Local Similarity 83. Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
NYPOPHETICAL 55.4 KDA PROPEIN IN IEO-IEI INTERGENIC REGION.
Autographa californica nuclear polyhedrosis virus (AcMNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00346; complex1_49xG; 1.
PROSITE; PS00535; COMPLEX1_49x; FALSE_NEG Ox1doreductase; NAD; Ubiquinone.
SEQUENCE 404 AA; 45675 MW; 638891610B0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
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30-MAY-2000 (Rel. 3)
30-MAY-2000 (Rel. 3)
NADH DEHYDROGENASE
STRAIN-C6;

MEDLINE-94303173; PubMed-8030224;

Ayres M.D., Howard S.C., Kuzio J.,

The complete DNA sequence of Auto
polyhedrosis virus.";

Virology 202:586-605(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AJ245399; CAB51632.1; -. InterPro; IPR001135; Complex1_49Kd.
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"Rhizobium meliloti carries two sets of nuo genes.";

Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

-I. CATALYTIC ACTIVITY: NADH + UBIQUINONE - NAD(+) + UBIQUINONE - NAD(+
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STRAIN-41;
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Bacteria; Proteobacteria; alpha subdivision;
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                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=46015;
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                                                                                                                                                                                                                                                                         EQUENCE FROM N.A.
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41700;
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el. 39, Last sequence update)
el. 39, Last annotation update)
el. 39, Last annotation update)
NASE I CHAIN D 2 (EC 1.6.5.3) (NADH-UBIQUINONE
CHAIN D 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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45675 MW; 638891610BC0A3EF CRC64;
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Pred. No. 52;
1; Mismatches
                                                                                           o J., Lopez-Ferber M., Possee R.D.;
Autographa californica nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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RESULT 10 PSAF\_HORVU

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RESCUENT RES
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Best Local
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032163;
30-MAY-2000
30-MAY-2000
20-AUG-2001
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                                                                                                                                                                                                                                                                 EMBL; 299120; CAB15257.1; -. SubtiList; BG14008; nifU. InterPro; IPR002871; NifU_N. Pfam; PF01592; NifU_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the E the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
FUNCTION: MAY BE INVOLVED IN THE FORMATION OR REPAIR OF
CLUSTERS PRESENT IN IRON-SULFUR PROTEINS (POTENTIAL).
-!- SIMILARITY: BELONGS TO THE NIFU FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
NCBI_TaxID-1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus subtilis.
Bacteria; Firmicut
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477 AA; 55417 MW;
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                                                                                                                                                                                                                        16166 MW;
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Pred. No.
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62;
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RESULT 11
THIL_PYRHO
ID THIL_P
AC 059497
DT 30-MAY
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Best Local Similarity 83.3
Matches 5; Conservative
THIL_PYRHO 059497;
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CONFLICT
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CONFLICT
SEQUENCE
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MEDLINE-90033290; PubMed-2680596;
Anandan S., Vainstein A., Thornber J.P.;
Correlation of some published amino acid sequences i polypeptides to a 17 kba LHCI pigment-protein and to IV of the core complex.*;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1990
01-JUN-1994
15-DEC-1998
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Scott M.P., Nielsen V.S.,
Submitted (MAR-1994) to t
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Eukaryota; Viridiplantae; Stro
Spermatophyta; Magnollophyta;
Triticeae; Hordeum.
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P13192;
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                                                                      194
                                                                                 1 REIIMD 6
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S Lett. 256:150-154(1989).

S Lett. 256:150-154(1989).

PUNCTION: PROBABLY PARRICIPATES IN EFFICIENCY OF ELECTRON TRANSFER PUNCTION: PROBABLY PARRICIPATES IN ELGAF AND FROM PLASTOCYANIN TO P700 (OR CYTOCHROME C553 IN ALGAE AND CYANDBACTERIA). THIS PLASTOCYANIN-DOCKING PROTEIN CONTRIBUTES TO THE SPECIFIC ASSOCIATION OF PLASTOCYANIN TO PS I.

TO THE SPECIFIC ASSOCIATION OF PLASTOCYANIN TO PS I.

SUBCELLULAR LOCATION: ASSOCIATED WITH LUMENAL SIDE OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE PSAF FAMILY.
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                                                                      REIIID 199
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(Rel. 37, Last sequence upda
I REACTION CENTRE SUBUNIT I
REACTION (PSI-F).
(Rel. 39, Created)
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                    STANDARD;
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235
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88
91
97
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yta; Liliopsida; Poales; Poaceae; Pooideae;
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                                                                                                                                                               CHLOROPLAST.
PHOTOSYSTEM I REACTION CENTRE SU
III.
C -> A (IN REF. 2).
S -> E (IN REF. 2).
F -> A (IN REF. 2).
REKQ -> HEQD (IN REF. 2).
REKQ -> HEQD (IN REF. 2).
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III PRECURSOR (LIGHT-HARVESTING
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Query Match
Best Local S
Matches 5
                                MEDLINE-98196666; PubMed-9537320;
Deckert G., Warren P.V., Gaasterland T., Young W.G., Le Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
"The complete genome of the hyperthermophilic bacterium aeolicus.";
                                                                                                                                                                                                                                                                                                                             066698;
20-AUG-2001
20-AUG-2001
20-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y., Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., N. Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohil Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oaki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K. Masuchi Y., Shizuya H., Kiuchi H.;

"Complete sequence and gene organization of the genome of a h thermophilic archaebacterium, Pyrococcus horikoshii OT3.";

"Day Bor S. 55.75.1000."
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pfam; PF00586; AIRS; 1.
Thiamine blosyothesis; Transferase
SEQUENCE 309 AA; 34348 MW; 771
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Archaea; Euryarchaeota;
NCBI_TaxID-53953;
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20-AUG-2001 (Rel. 40, Last annotation update)
PROBABLE THIAMINE-MONOPHOSPHATE KINASE (EC 2.7.4.16) (THIAMINE-PHOSPHATE KINASE)
PHOSPHATE KINASE)
THIL OR PH1833
                                                                                                                                                                                                                   Bacteria; Aquificales;
NCBI_TaxID=63363;
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Bacteria; Aquific
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Nature 392:353-358(1998).
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SIMILARITY: BELONGS TO THE THIAMINE-MONOPHOSPHATE KINASE FAMILY
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5; Conservative
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(Rel. 40,
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34348 MW; 771B841B267F6511 CRC64;
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AQ_376.
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Pred.
1; Mis
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                                                                bacterium
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                                                                                                     Lenox A.L.,
ly M., Huber
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Ohfuku Y.,
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INTEGRAL

MEMBRANE PROTEIN (POTENTIAL)

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RESULT 13
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Nagase 7., Ishikawa K.-I., Suyama M.,

Najalima N., Tanaka A., Kotani H., Nomura N., Ohara O.;

"Prediction of the coding sequences of unidentified human genes. XIII.

"The complete sequences of 100 new cDNA clones from brain which code

"I for large proteins in vitro.";

LDNA Res. 6:63-70(1999).

LDNA Res. 6:63-70(19
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TRANSMEM 81 103
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SEQUENCE
                                                                                This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
FYVE FINGER-CONTAINING PHOSPHOINOSITIDE KINASE (EC 2.7.1.68) (1-
PHOSPHATIDYLINOSITOL-4-PHOSPHATE KINASE) (PIP5K) (PTDINS(4)P-5-KINASE)
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                  EMBL; AB023198; BAA76825.1; -. InterPro; IPR002498; PIP5K.
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HSSP; p07157; har.

InterPro; IPR000640; EFG_C.

& InterPro; IPR000795; GTP_EFTU.

& Pfam; pF00679; EFG_C; 1.

PFam; pF00009; CTP_EFU; 1.

PR Pfam; pF00009; CTP_EFU; 1.

PROSITE; PS00301; EFACTOR_GTP; 1.

PROSITE; PS00301; EFG_C.

PROSITE; PS00301; EFACTOR_GTP; 1.

PROSITE; PS00301; EFG_C.

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P14823;
01-APR-1990 (Rel. 1
01-APR-1990 (Rel. 1
20-AUG-2001 (Rel. 4
ELONGATION FACTOR 2
                                                                                                            Elongation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Sequence analysis of the peptide-elongation factor EF-2 gend
downstream from those of ribosomal proteins H-S12 and H-S7,
archaebacterial extreme halophile, Halobacterium halobium.";
Eur. J. Biochem. 186:213-219(1989).
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Transferase; Kinase.
NON_TER 1 1
SEQUENCE 578 AA; 645
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Archaea; Euryarchaeota;
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         Score 25; DB
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Pred. No. 1.4e+02,
2; Mismatches (
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RESULT 15
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R EMBL; 299091; CAB11774.1; -.

R InterPro; IPR002863; MutS_C.

R InterPro; IPR002863; MutS_C.

R Pfam; PF01624; MutS_C; 1.

R Pfam; PF01624; MutS_C; 1.

R PrODom; PD001263; MutS_C; 1.

R PrODom; PD001263; MUTS_C; 1.

R PROSTITE; SM00534; MUTSSG; 1.

R SMART; SM00534; MUTSG; 1.

R PROSITE; PS00486; DNA_MISMATCH_REPAIR_2; 1.
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013921; 013700;
15-DEC-1998 (Rel. 37, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
MUTS PROTEIN HOMOLOG 1.

SPAC23C11.18C OR SPAC13F5.01C.
SCh1zosaccharomyces pombe (Fission yeast).
Sch1zosaccharomycetales; Sch1zosaccharomycetes;
Sch1zosaccharomycetales; Sch1zosaccharomycetaceae;
Sch1zosaccharomyces.
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249 REIVLD 254
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-i- FUNCTION: INVOLVED IN MITOCHONDRIAL DNA REPAIR (POTENTIAL).
-i- SIMILARITY: BELONGS TO THE DNA MISMATCH REPAIR MUTS FAMILY.
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US-09-544-665-4 29 1 REIIMD 6

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March 18, 2002, 09:51:57

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Scoring

table: score:

BLOSUM62 Gapop 10.0 , Gapext 0.5

473505 seqs, 146272329 residues

Minimum Maximum

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Database

SPTREMBL\_17:\*

sp\_archea:\*
sp\_bacteria:\*

sp\_organelle:\*
sp\_phage:\*
sp\_plant:\*

sp\_rodent:\*
sp\_virus:\* sp\_vertebrate:\*
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sp\_mammal:\*
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Copyright (c) 1993 - 2000 Compugen
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09ax28 oryza sativ
026642 methanbact
09ru01 deinococcus
09ac56 caulobacter
09zcy7 rickettsia
097916 bos taurus
012230 saccharomyc
064796 autographa
0911h9 frog adenov
092494 bombyx mori
027657 giardia lam
09ku86 vibrio chol
09tuq1 bos taurus
09tuq1 bos taurus
09tuq1 sos taurus
                                                                                                                                                                                                                                              057935 methanococc 016391 caenorhabdi 09ma55 arabidopsis 09ch00 lactococcus 059606 pyrococcus
                                                                                                                                                                                                                                                                                                                                                        Description
 RP SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

RC STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

RC STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

RX MEDLINE-95337999; PubMed-8688087;

RA BUIT C.J. White O., Olsen G.J., Zhou L., Fleischmann R.D.,

RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

RA Scott J.L., Geoghagen N.S.M., Weidman J.E., Puhrmann J.L., Nguyen D.,

RA Scott J.L., Geoghagen N.S.M., Weidman J.D., Sadow P.W., Hanna M.C.,

RA Scott J.L., Geoghagen N.S.M., Weidman J.D., Sadow P.W., Hanna M.C.,

RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,

RT "Complete genome sequence of the methanogenic archaeon, Methanococcus

RT Jannaschii.",

Science 273:1058-1073(1996).

CC -1- COACTOR: MICKEL (BY SIMILARITY).

CC -1- SUBUNIT: FHL COMPRISES OF A FORMATE DEBYDROGENASE, UNIDENTIFIED

CC -1- SUBUNIT: FHL COMPRISES OF A FORMATE DEBYDROGENASE, UNIDENTIFIED

CC -1- SUBUNIT: FHL COMPRISES OF A FORMATE (BY SIMILARITY).

CC -1- SUBUNIT: BELONGS TO THE COMPLEX (JS KDB SUBUNIT FAMILY.

DR FORMATE ARE RELEASED (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE COMPLEX I 49 KDA SUBUNIT FAMILY.

DR TIGR; MJ0515; -- Complex! 49Kd.

DR TIGR; MJ0515; Complex! 49Kd.
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Q57935;
Q57935;
Q57936;
Q1-JAN-1998 (TIEMBLIEL 0
Q1-JUN-2001 (TIEMBLIEL 0
Q1-JUN-2001 (TIEMBLIEL )
PUTATIYE FORMATE HYDROGEN
3 COMPONENT E).
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InterPro; IPR001135; Complex1_49Kd.
InterPro; IPR001501; NiFeSe_Hases.
Pfam; PP00346; complex1_49Kd; 1.
Pfam; PP00374; NiFeSe_Hases; 1.
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Archaea; Euryarchaeota; Methanococcales;
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MBLrel. 17, Last annotation update)
HYDROGENLYASE SUBUNIT 5 (FHL SUBUNIT 5) (HYDROGENASE-
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09v8m4 drosophila
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09z630 streptococc
09z65 sphingomona
09z4w8 pseudomonas
09z4w8 pseudomonas
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09a25 caulobacter
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016391;
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01-NOV-1998 (TIEMBLIEL:
01-JUN-2001 (TIEMBLIEL:
                                                                                                                                                                                                                                                                                                                                                                                                   Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston I
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownker
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mof contiguous nucleotide sequence from chromosome III of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-94150718;
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PROSITE; PS00507; NI_HGENASE_L_1; UNKNOWN_1
Hypothetical protein; Oxidoreductase; NAD;
Nickel; Complete proteome.
SEQUENCE 380 AA; 43638 MW; 3EAD16D67834
                                                                                                                                                                                                                                                                                         *The sequence of C. elegans
Submitted (AUG-1997) to the
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Rhabditidae; Peloderinae;
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t Local Similarity
ches 6; Conserv
                       Pfam; PF00104; hormone_rec; 1. Pfam; PF00105; zf-C4; 1. PRINTS; PR00047; STROIDFINGER.
                                                                                          Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: TO C4-TYPE STEROID RECEPTOR ZINC FINGER EMBL; AF016443; AAC24282.1; -.
HSSP: P03372: 1HCP.
                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                      Submitted (JUL-1997)
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
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                                                                    InterPro;
InterPro;
                                                                                                                                                                Waterston R.;
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SM00430;
SM00399;
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IPR001628;
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 ZnF_C4;
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zf-C4.
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EMBL/GenBank/DDBJ databases.
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No.
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                      SEQUENCE FROM N.A.
STRAIN-IL1403;
Bolotin A., Wincker P., M
Weissenbach J., Ehrlich S
"The complete genome sequ
                                                                                                                                                                                                                                                                                                                                                                                                                          Q9CH00;
01-JUN-2001
01-JUN-2001
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01-OCT-2000
01-OCT-2000
01-OCT-2001
01-JUN-2001
F22F7.13 PROF
F22F7.13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D., Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E., Bownan C.L., White O., Nierman W.C., Fraser C.M.; "Arabidopsis thaliana chromosome III BAC F22F7 genomic sequence."; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AC009606; AAR64540.1; -.

InterPro; IPR007582; ACBP.
InterPro; IPR00798; Kelch.

Pfam; PP001344; Kelch; 5.
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Zinc-finger.
SEQUENCE 413 AA; 47387 MW;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID-3702;
                                                                                                                                                                                                                                                                                         Lactococcus lactis (subsp. lactis) (Streptococcus Bacteria; Firmicutes; Bacillus/Clostridium group;
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                                                                                                                                                                                                                          Lactococcus.
NCBI_TaxID=1360;
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AK KAWATABAYASI Y., SAWAGA M., HOTIKAWA H., HOSOYAMA A., NA9AI Y.,

AK YAMAMOKO S., Sekine M., Baba S.-I., KOSUYI H., HOSOYAMA A., NA9AI Y.,

AK SAKAI M., OGUTA K., OTSUKA R., NAKAZAWA H., TAKAMIYA M., OHUKU Y.,

AK FUNAHASHI T., TANAKA T., KUGOH Y., YAMAZAKI J., KUSHIGA N., OGUCHI A.,

AKAKI K.-I., YOSHIZAWA T., KUGOH Y., YAMAZAKI J., KUSHIGA N., OGUCHI A.,

AKAWATABASHI T., TANAKA T., KUGOH Y., YAMAZAKI J., KUSHIGA N., OGUCHI A.,

AKAWATABASHI T., KIKUCHI H.;

COMPLETE SEQUENCE AND GENE OF GRANITATION OF THE GENOME OF A hyper-

THE THE SEQUENCE AND GENERAL TO THE SECUENCY OF THE S
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EMBL; AB006338; AAK05040.1; -.

InterPro: IPR001900; Ribonuclease_II.

InterPro: IPR003029; S1.

Pfam: PP00773; RNB; 1.

Pfam: PP00775; S1; 1.

SMART; SM00316; S1; 1.

PROSITE; PS01175; RIBONUCLEASE_II; 1.

PROSITE; PS01175; RIBONUCLEASE_II; 1.

Complete proteome.

SEQUENCE 817 AA; 92250 MW; 44079115
01-JUN-2001
01-JUN-2001
P0456A01.7 P
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01-AUG-1998
01-JUN-2001
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NCBI_TaxID=53953;
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Archaea; Euryarchaeota
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(TrEMBLrel. 07, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
. 28.0 KDA PROTEIN PH1943.
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1; Mismatches
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Pred. No. 3e+02;
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01-JAN-1998 (TrEMBLrel. 0)
01-JAN-1998 (TrEMBLrel. 0)
01-MAR-2001 (TrEMBLrel. 1)
CONSERVED PROTEIN.
  Q9RU01;
Q9RU01;
01-MAY-2000
01-MAY-2000
01-JUN-2001
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., DuBois Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., DuBois Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Yiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-1., Rice P., Nolling J., Reeve J.N.; "Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics."; J. Bacteriol. 179:7135-7155(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
"Clone:P0456A01.";
"Submitted (CCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP002899; BAB21151.1;
"EMBL; AP0028999; BAB21151.1;
                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome. SEQUENCE 437 AA;
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Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
Methanothermobacter.
NCBI_TaxID-145262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-DELTA H;
MEDLINE-98037514; PubMed-9371463;
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STRAIN-CV. NIPPONBARE;
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  (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                       Score 27;
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Matches 4
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Q9AC56;
Q1-JUN-2001
01-JUN-2001
01-JUN-2001
                                                                   MEDINE=21173698; PubMed=11259647;

Nierman W.C., Felddblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

Elsen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.

Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

"Complete genome sequence of Caulobacter crescentus.";

Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

EMBL, AE005675; AAKZ1993.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001282; G6PD.

Pfam; PF00479; G6PD; 1.

PRINTS; PR00079; G6PDHDRANASE.

ProDom; PD001129; G6PD; 1.

PROSITE; PS00069; G6P_DEHYDROGENASE; 1.

COmplete proteome; Glucose metabolism; NADP; Oxidoreductase.

SEQUENCE 590 AA; 65600 MW; DA42AEBB4D277722 CRC64;
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01-JUN-2001 (TEMBLIE1. 17, Last seq
01-JUN-2001 (TEMBLIE1. 17, Last sen
01-JUN-2001 (TEMBLIE1. 17, Last sen
01-MP POLYMERASE III, EPSILON SUBUNIT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1 .; radiodurans R1 .; Science 286:1571-1577(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caulobacter crescentus
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proteome.
237 AA;
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SPHATE + NADPH
WW;
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Last annotation update)
SUBUNIT
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Best Local S
Matches 5
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O97916;
O1-MAY-1999 (TrEMBLrel. 10, C
O1-MAY-1999 (TrEMBLrel. 17, L
O1-JUN 2001 (TrEMBLrel. 17, L
REVERSE TRANSCRIPTASE-LIKE.
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O9ECY7;
O9ECY7;
O1-MAY-1999 (TrEMBLrel. 10, Created)
O1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
O1-MAY-2000 (TrEMBLrel. 13, Last annotation updat
""POTHETICAL 37.5 KDA PROTEIN.
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STRAIN-MADRID E;

MEDLINE-99039499; PubMed-9823893;

Andersson S.G.E., Zomorodipour A., Andersson J.O.,

Alsmark U.C.M., Podowski R.M., Naeslund

Briksson A.-S., Winkler H.H., Kurland C.G.;

"The genome sequence of Rickettsia prowazekii and the origin

mitochondria.";
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Merinckx A., Mercier D., Oulmouden A., Petit J.M., Julien "Complete genomic organization of bovine futb gene reveals 5'-untranslated exons of FUT3 and FUT6 have recently emerge ancestral intronic sequences.";

Submitted (FEB-199) to the EMBL/GenBank/DDBJ databases.

-I- SIMILARITY: TO RNA-DIRECTED DNA POLYMERASE (REVERSE TRANSCRIPTASE).

EMBL; AJ132772; CAA10770.1;

InterPro: IPR000477; RVTse.
                                                                                                                                                                                                                                                                                                                                                                                                                                         RTLF.
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi,
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi,
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Boyinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 396:133-140(1998),
EMBL; AJ235272; CAAI5012.1; -.
Hypothetical protein; Complete
SEQUENCE 327 AA; 37453 MW;
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NCBI_TaxID=782;
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Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
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nes 5; Conservative
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1; Mismatches
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Best Local Similarity
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Badcock K., Bowman S., Ch
Walsh S.V., Barrell B.G.;
Walsh Apr. 1996) to t
                                                                                                                           Hall J. Ahmed A., Bussey H., Fortin N., Friesen J.D., Vo D.H., Wang Y. Winett E.: Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases EMBL; Z71255; CAA95037.1; -. EMBL; Z46483; CAA88302.1; -. EMBL; U3335; AAB68101.1; -. SGD; S0005925; YPL004C.
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-91092258; PubMed=2265610;
MEDLINE-91092258; PubMed=2265610;
Gerring S.L., Spencer F., Hieter P.;
Gring F. Gerring S. Gerring S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q12230
Q12230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDLINE-89057455; PubMed-3143101;

O'Hara P.J., Horowitz H., Eichinger G., Young
O'Hara P.J., Horowitz H., Eichinger G., Young
"The yeast ADR6 gene encodes homopolymeric am:
potential metal-binding domain.";
Nucleic Acids Res. 16:10153-10169(1988).
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01-NOV-1996 (TrEMBLrel. 01, Last seque
01-MAR-2001 (TrEMBLrel. 16, Last annot
HYPOTHETICAL 38.1 KDA PROTEIN YPL004C.
PYPL004C OR LPA13C.
                                                                                      Hypothetical protein SEQUENCE 341 AA;
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Walsh S.V., 1
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Badcock K., C
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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RNA-directed DNA polymerase.
SEQUENCE 335 AA; 38403 MW;
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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Last sequence update)
Last annotation updat
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Pred. No. 3.4e
2; Mismatches
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    Score
Pred.
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                                                                                           6FCEE022ECC9778C CRC64;
       26;
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       DB 3;
3.5e+02;
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RESULT
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AC Q64796
AC Q6

RESULT
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ID 09
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DT 01
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092494 I
092494;
01-NOV-1998 (
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Q911H9;
01-OCT-2000
01-OCT-2000
01-JUN-2001
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Q64796;
Q1-NOV-1996
Q1-NOV-1996
Q1-AUG-1998
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

Bavison A.J., Wright K.M., Harrach B.;
pavison A.J., Wright K.M., Harrach B.;
"phylogenetic position of an amphibian adenovirus.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF224336; AAF86928.1;
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EMBL, AF26436; AAF86928.1;
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EMBL, FP10168; Adeno_Penton_B.

1.

SEQUENCE 445 AA; 50029 NM; E5061EFB041CB0CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Frog adenovirus 1.
Viruses; dsDNA viruses,
NCBI_TaxID=114102;
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Submitted (DEC-1993) to the EMBL/GenBank/DDBJ da
EMBL; U04051; AAA0535.1; -
SEQUENCE 425 AA; 49374 MW; 7572BD3EBC6B2A52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Autographa californica :
Viruses; dsDNA viruses,
Nucleopolyhedrovirus.
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pred. No. 4.7e+02;
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1; Mismatches
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Page 6
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DT 01-NOV-1998 (TREMBLTel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBLTel. 08, Last annotation update)
DE ACMNEV ORF142.
OS BOMBYX MOTI Nuclear polyhedrosis virus (BmNPV).
OC VIRUSES; d5DNA VIRUSES, NO RNA Stage; Baculoviridae;
OX NCBL_TaxID=10458;
RN 121
RP SEQUENCE FROM N.A.
RC STRAIN=73;
RX MEDLINE-97329351; PubMed=9185864;
RA KAMILA S.G., Maeda S.;
RA KAMILA S.G., Maeda S.;
RT "Sequencing of the putative DNA helicase-encoding gene of the Bombyx mori nuclear polyhedrosis virus and fine-mapping of a region involved for nuclear polyhedrosis virus and fine-mapping of a region involved rate for the putative DNA helicase-encoding gene of the Bombyx mori nuclear polyhedrosis virus and fine-mapping of a region involved for polyhedrovirus.";
RN 5EQUENCE FROM N.A.
RC STRAIN=73;
RA SQUENCE FROM N.A.
SGOUTE S., Majima K., Maeda S.;
RA SQUENCE FROM N.A.
SGOUTE S., Majima K., Maeda S.;
RA SQUENCE GALLYIUS of the genome of Bombyx mori rucleopolyhedrovirus.";
RA SQUENCE 476 AA: 55375 MM; ACOEGO102260906B CRC64;
Ouery Matches 5; Conservative 1; Mismatches 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps
Oy 1 REIIMD 6
Db 320 REIILD 325
Search completed: March 18, 2002, 09:51:59
Job time: 288 sec
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence:
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Perfect score:
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                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                         Score
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Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  March 18, 2002, 09:48:56; Search time 81.32 Seconds (without alignments) 5.465 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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/SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:*
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                                                      AAY01814
AAB95262
AAW84351
AAB31162
AAW10344
AAG98338
AAR82886
AAW31227
                                                                                                                                                                                                                                                         SUMMARIES
Peptide used to re Human protein seque Murine ubiquitin-p Amino acid sequenc Maize dwarf mosaic Escherichia coli p Human leucine zipp Human leucine-zipp Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia
                                                                                                                                                                                                     Description
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AAY01814
       Cines D,
                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                      Abnormal cell migration; PAI-1-dependent cell adhesion; scuPA clearance; pathological cell migration; angiogenesis; organogenesis; ovulation; inflammation; cancer; tumor cell invasion; metastasis; atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY01814 standard; peptide; 6 AA
                                                                                   WPI; 1999-288168/24
                                                                                                                                                                                      17-OCT-1997;
                                                                                                                                                                                                                                                       29-APR-1999.
                                                                                                                                                                                                                                                                                       WO9920295-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY01814;
                                                    Peptide composition
                                                                                                                                                                                                                      15-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide used to regulate scuPA.
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Human ST-S1, used	AAW08084	17	282	82.1	23	5
Mouse ST-S1, used	AAW08083	17	281	82.1	23	4
-	AAG47105	21	273	82.1	23	ω
thali	AAG23339	21	273	82.1	23	N
ei	AAM01058	22	240	•	23	ш
Arabidopsis thalia	AAG32040	21	236	82.1	23	0
æ	AAY20032	20	223		23	9
Arabidopsis thalia	AAG32041	21	220	•	23	8
Growth factor rece	AAW18063	18	217	•	23	7
	AAY20033	20	198	•	23	σ
	AAY48261	20	187	•	23	ر.
Human secreted pro	AAG01421	21	152	•	23	4
Human 5' EST secre	AAY12378	20	138	٠	23	w
Retrotransposon co	AAY50790	21	137	•	23	Ν
	AAY12851	20	47	•	23.	ר
Thrombin inhibitor	AAB92200	22	33	•	23	0
Ļ	AAY42738	20	33	•	23	9
N-terminal t-PA in	AAR26000	13	19		23	80
ã	AAY01812	20	6	•	23	7
	AAB62448	22	1698		24	σ
	AAY34434	20	973	•	24	ū
phorymonas	AAY34577	20	961	•	24	4
=	AAB69348	21	860	•	24	ũ
1 gp120 prote	AAW43080	19	859	•	24	N
HIV-1 gp120 protei	AAW43077	19	853		24	ت
HIV-1 non-subtype	AAB69353	21	846		24	Ö
	AAR08406	1	846		24	٥
ino acid sequ	AAY29146	20	811		24	8
	AAW98595	19	378	•	24	7
	AAY81704	21	329	•	24	6
Streptococcus pneu	AAY81702	21	314		24	Ċ1
B. thuringiensis t	AAW60180	19	306	85.7	24	4
Transposon Tn5401	AAR69825	16	306		24	w
Canine interleukin	AAW95359	20	265	85.7	24	Ν

## ALIGNMENTS

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Example 1; Page 31; 63pp; English
                                                                                                                                     (UYPE-) UNIV PENNSYLVANIA.
                                                                                                    Higazi AA;
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Matches
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11-JAN-2000;
02-MAY-2000;
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Ishii :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptides AAY01812-14 exemplify the peptide of the invention, which is used in a peptide composition to affect a biological process characterized by abnormal cell migration through a physiological barrier, to inhibit PAI-1-dependent adhesion of a cell to a tissue, to promote clearance of scuPA from the surface of a mammalian cell, and to impede pathological migration of a cell in a mammal. The composition can be used to affect a biological process characterized by abnormal cell migration through a physiological barrier, where the process is selected from anglogenesis, organogenesis, oventation, inflammation, cancer, tumor cell invasion and metastasis, and atherosclerosis.
The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of $602$ nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 5'-end sequence which comprises a 5'-end sequence complementary to a polynucleotide which comprises a 5'-end sequence complementary to a polynucleotide which comprises a 5'-end sequence complementary to a polynucleotide which comprises a 5'-end sequence complementary to a polynucleotide which comprises a 5'-end sequence complementary to a polynucleotide which comprises a 5'-end sequence complementary to a polynucleotide comprises a 5'-end sequence complementary to the comprise complementary to the comprise and an oligonal comprise complementary to the comp
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                                                                                                                                                                                                                                                                                 Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
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                                                                                                                                                                                                                                          Claim
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6; Conserv
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, Sugiyama
                                                                                                                                                                                                                                       SEQ ID 17446; 2537pp +
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2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             detection; diagnosis; antisense therapy; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                        Nishikawa T,
T, Wakamatsu
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                                                                                                                                                                                                                                          CD ROM; English
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A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               No.
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K, Otsuki
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                                                  The present sequence represents a ubiquitin-protein ligase called The Ubrl enzymes are involved in protein ubiquitinylation and ultimate degradation through the N-end rule pathway and have been linked to stress-related muscle wasting. Recombinant Ubrl polypept can be used to screen for inhibitors of muscle wasting when this i associated with the N-end rule pathway.
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                                                                                                                                                                                                                                                             Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kwon YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-DEC-1997;
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      Sequence
                                                                                                                                                                                                                                                                                                                   polypeptides
                                                                                                                                                                                                                                                                                                                                         Mouse and human Ubr1 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CALY ) CALIFORNIA INST OF TECHNOLOGY.
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5; Conserv
      1757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              401
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                                                                                                                                                                                                                                                             Columns 15-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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      ξ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ?
                                                                                                                                                                                                                                                             18pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 27; DB Pred. No. 1.56
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                   useful for producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          muscle wasting; inhibitor; screen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 22; I
1.5e+02;
ches 0;
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                                                                                                                                                                                                                                                                                                                                                      recombinant
                                                                                        polypeptides
en this is
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Query Match Best Local S Matches 5

Similarity 83. 5; Conservative

96.4%;

Score 27; DB Pred. No. 6.7e 1; Mismatches

DB 20; .7e+02; es 0;

Length 1757;

Indels

0

Gaps

0

Maize dwarf mosaic virus polyprotein

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RESULT
AAW10344
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AAB31162
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                                       ä
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                                                                                                                         Query Match 96.7
Best Local Similarity 83.7
Matches 5; Conservative
                                                                                                                                                                                                             The present sequence represents a murine Ubrl enzyme. Ubrl is an E3-type protein of the ubiquitin system. Specifically, it is a ubiquitin protein ligase. The enzyme is specific for destabilising residues exposed at the N-terminus of protein substrates. Inhibition of the expression of Ubrl gene in a cell results in inhibition of the N-end rule pathway. The method is used for treatment of mammalian cells infected with an intracellular pathogen, e.g. Lysteria monocytogenes or Yersinia entercolitics. Inhibition of N-end rule pathway is also useful for
                                                                                                                                                                                                                                                                                                                     Inhibiting the N-end rule pathway in mammalian cells for treating infections and various diseases associated with muscle tissue wasting, by inhibiting the expression of Ubrl gene
 15-APR-1997
                  AAW10344;
                                    AAW10344 standard;
                                                                                                                                                                          Sequence
                                                                                                                                                                                                enterocolitica. Inhibition of N-end rule painway is also usely. ... treating various diseases associated with wasting of muscle tissue and
                                                                                                                                                                                                                                                                                                    Example; Column 15-28; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                        Kwon YT, Varshavsky A;
                                                                                                                                                                                                                                                                                                                                                                                                            (CALY ) CALIFORNIA INST OF TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                02-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ubrl; E3-type protein: ubiquitin system: ubiquitin-protein ligase;
N-end rule pathway; intracellular pathogen; Lysteria monocytogenes;
Yersinia enterocolitica; muscle wasting; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid sequence of Mouse Ubrl protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB31162;
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||:|||
765 eevimr 770
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                                                                                   765 eevimr 770
                                                                                                        1 EEIIMR 6
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DB; AAC86933.
                                                                                                                                                                          1757 AA;
(first entry)
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                                    Protein; 2763 AA
                                                                                                                          Score 27; DB Pred. No. 6.7e
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                                                                                                                                   DB 22;
6.7e+02;
                                                                                                                           0,
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                                                                                                                          Indels
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 (CIBA ) CIBA GEIGY
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/note=
Misc-difference 852
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Misc-difference 712
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                                                                                                                                                                                                                                                                                                                                                                            /label= Coat_protein
30-JUN-1995;
                                                                                                              Misc-difference
                                                                                                                                      Misc-difference
                                                                                                                                                        /note=
Misc-difference 1362
                                                                                                                                                                           /note=
Misc-difference 1346
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Misc-difference 847
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Misc-difference 843
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Misc-difference 834
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Misc-difference 829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MDMV-B; viral resistance; disease resistance; transgenic plant; monocot; P3 proteinase; NIa proteinase; NIb replicase; RNA-dependent RNA polymerase; coat protein; Zea mays; sorghum; sugarcane; Saccharum officinale.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein
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                       20-JUN-1996;
                                                 23-JAN-1997
                                                                         W09702352-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maize dwarf mosaic virus strain B.
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 95US-0496944
                          96WO-EP02673.
                                                                                                             /note=
2385
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2077
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/note* "portion of the helper component-P2
proteinase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                       /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= NID_replicase
/note= "claimed polypeptide (Claim 20)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= NIa_proteinase
/note= "claimed polypeptide (Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Cylindrical_inclusion_protein
/note= "claimed polypeptide (Claim 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  label= P3_proteinase
note= "claimed polypeptide (Claim 20)"
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                                                                                                                                                                                                                                                                                                                                                                                                                        "conserved motif characteristic of
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence of the polyprotein encoded by the polycistronic mRNA (AA747073) of maize dwarf mosaic virus strain B (MDMV-B) is given in AAM10344. New chimaeric genes comprise a monocotyledonous plant promoter linked to a modified nucleic acid sequence derived from the MDMV-B genome. The modification is such that mRNA is translated to a truncated protein (pref. smaller than 200 amino acids), no translation of mRNA occurs or the transcribed mRNA lacks the translation initiation codon or includes a premature stop codon. Expression of the chimaeric gene inhibits infection of plants (pref. sorghum, sugarcane, esp. maize) by MDMV. The transgenic plants display an inheritable resistance trait.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; Page 31-44; 64pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimaeric gene for imparting viral resistance to plants - contains sequence modified to express non-translatable mRNA, or non-coat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dietz JM,
                                                                                                                                                                                                                                                             05-JUL-2001
                                                                                                                                                                                                                                                                                                                     Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                              Escherichia coli; identification; proliferation; microorganism;
antimicrobial; antibacterial; antibiotic; gene therapy; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli protein sequence SEQ ID NO:386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG98338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG98338 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2064 eeivmr 2069
                          Claim 19; Page 507-508; 596pp; English.
                                                                                                                                                                                                                                19-DEC-2000; 2000WO-US34419
                                                                                                                                                                                                                                                                                           WO200148209-A2
                                                                                                                                                                                                                                                                                                                                                bacterial growth inhibition
                                                                                                                                                                                                                                                                                                                                                                                                                                    21-SEP-2001 (first entry)
                                                     Novel nucleic acids encoding proteins required for Escherichia proliferation, useful for screening for antimicrobial agents -
                                                                                                N-PSDB; AAH81394.
                                                                                                               WPI; 2001-457376/49.
                                                                                                                                            Forsyth RA,
                                                                                                                                                                        (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EEIIMR 6
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DB; AAT47073.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2763 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                            Ohlsen KL,
                                                                                                                                                                                                    99US-0173005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96.4%;
                                                                                                                                            Zyskind JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                246
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Pred. No. 1.1e+03;
1; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 2763;
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                                                                      coli
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The present invention describes a purified or isolated nucleic

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene therapy. Expression of (1) in a microorganism inhibits proliferation of the microorganism, and the manufactured antibiotic is useful for reducing the activity or level of a gene product required for proliferation of a microorganism in a subject, specifically humans. The nucleic acids that inhibit bacterial growth or proliferation can be used as antisense therapeutics for killing bacteria. In addition to therapeutic applications, the nucleic acid sequences complementary to sequences required for proliferation can be used as diagnostic tools. For example, nucleic acid probes complementary to proliferation required sequences that are specific for particular species of microorganisms can be used as probes to identify particular microorganism species in clinical specimens. AAH81295 to AAH81487 encode the Escherichia coli proteans given in AAG89239 to AAK894431, and AAH81488 to AAH81491 of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence (I) consisting essentially of one of the 93 nucleotide sequences given in AAH81202 to AAH81294, where expression of the nucleic acid in a microorganism is capable of inhibiting proliferation of a microorganism.

(I) have antibacterial and antibiotic activities, and can be used in
           This novel protein may be used to treat tumors of the CNS in mammal by inhibiting the overexpression of the leucine zipper protein-kinase in vivo, or by interfering with a vital signal in a chain of signals leading to tumorigenicity.
                                                                                                                          DNA encoding novel leucine zipper polypeptide(s) prepared using the hyper-proliferation of CNS cells
                                                                                                                                                                                            WPI; 1995~320565/41.
N-PSDB; AATO1031.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leucine zipper protein-kinase; enzyme; zpk; CNS; diagnosis; central nervous system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                            Claim 4; Page 23-27; 40pp; English.
                                                                                                                                                                                                                                              Pleasure DE,
                                                                                                                                                                                                                                                                            (CHIL-) CHILDRENS HOSPITAL PHILADELPHIA.
                                                                                                                                                                                                                                                                                                             01-MAR-1994;
                                                                                                                                                                                                                                                                                                                                             28-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                              08-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                             W09523849-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human leucine zipper protein-kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR82886;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR82886 standard; Protein; 859 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               represent oligonucleotides, which are used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EEIIMR 6
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5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               246 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                           Reddy
                                                                                                                                                                                                                                                                                                             94US-0205018.
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Pred. No. 2.6e+02;
1; Mismatches 0
                                                                                                                                              protein kinase - also probe(s)
DNA, useful for inhibiting
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RESULT
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Misc-difference 292
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Misc-difference 278..280
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Misc-difference 254..256
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Misc-difference 236..237
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                                                                                                                                                                                                                                                                                                                                       Region
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             US5676945-A
                                                                                 Region
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/label= I
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234_235
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                                                                                                                                                                                                                                                                                                                                       /note= "Mentioned in specification" 415..418
                                                                                                                                                                                                                                                                                                 /note- "Putative endoplasmic reticulum targeting sequence as given in the specification"
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"As stated in specification"
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Pred. No. 9.4e
2; Mismatches
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9.4e+02;
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25-FEB-1999;
                                 25-FEB-2000;
                                                                   06-SEP-2000
                                                                                                       EP1033405-A2
                                                                                                                                         Arabidopsis thaliana
                                                                                                                                                                           termination sequence.
                                                                                                                                                                                           Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                 Arabidopsis thaliana protein fragment SEQ ID NO:
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94US-0205018.
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Pred. No. 9.4e+02;
2; Mismatches 0;
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                                                                                                                                   Arabidopsis thaliana.
                                                                                                                                                    Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control; termination sequence.
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Similarity 83.3%;
5; Conservative
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990S-0158232
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Pred. No. 1.2e+03;
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hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.
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The invention relates to a human interleukin (IL)-1 alpha propiece polypeptide. The polypeptide has activity in the selective induction of apoptosis in cancer cells. The IL-1 alpha propiece polypeptide or its variants which retain the apoptosis-inducing activity are used in compositions and methods to selectively induce apoptosis in cancer cells, especially manignant cancer cells. The polypeptides form the basis for especially manignant cancer cells where apoptosis-inducing agents
                                                                                                                        New polypeptides comprising an apoptosis-inducing domain and a heterologous nuclear localisation sequence - useful for, e.g. forming compositions and methods for selectively inducing apoptosis in cancer cells
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30-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                      Interleukin;
cancer; cell
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                                                                                                 Disclosure;
                                                                                                                                                                                   WPI; 1999-059804/05
                                                                                                                                                                                                           Lovett DH,
                                                                                                                                                                                                                                  (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                          28-MAY-1998;
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5; Conservative
                                                                                               Page 65-66; 88pp; English.
                                                                                                                                                                                                           Pollock AS,
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Pred. No. 1.4e+03;
1; Mismatches 0;
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Score 24; DB Pred. No. 5.6e 2; Mismatches

.6e+02; 0.

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                                                      Tn5401 is present in B.t. var. morrisoni strain E0218 (NRL-B-18213). E02158 was transformed with donor plasmid pE0911 and recombinant plasmids were analyzed. 2 Contained a 5 kb insert (given in AAQ85492) including 2 ORFs encoding a resolvase (AAR69825) and a transposase (AAR75354). Tn5401 is used in site-specific recombination to construct improved B.t. strains for biological
                                                                                                                                                                                                  Disclosure; Page 49-58; 106pp;
                                                                                                                                                                                                                                    New transposon {\tt Tn5401} from Bacillus thuringiensis and fragments of it - and related plasmids and transformed B. thuringiensis useful as insecticides
                                                                                                                                                                                                                                                                                                                        WPI; 1995-066902/09.
N-PSDB; AAQ85492.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-JUL-1993;
24-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transposon; Tn5401; resolvase; insecticide; biological control agent; site-specific reco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-JUL-1994;
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94US-0266408.
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66.7%;
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                                                                                                                                                                                                    English.
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recombination;
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AAY81702
ID AAY8
                                                                                                                                                                                                                                                                                                                                  thuringlensis transposon Th5401. The transposable element Th5401 concerns the concess of the control of the con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-SEP-1996;
08-JUL-1993;
24-JUN-1994;
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  AAY81702 standard; Protein; 314 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This represents the resolvase protein encoded by tnpI of the Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Fig 1A-L; 57pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Insecticidal recombinant Bacillus thuringiensis strains - contain transposable elements for expression of recombinant insecticidal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-397942/34.
N-PSDB; AAV34699.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-SEP-1998 (first entry)
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Pred. No. 5.6e
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.5.6e+02;
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This sequence represents a Streptococcus pneumoniae protein of the cinvention. The proteins (or their homologues, derivatives and/or cragments) are useful as immunogens or antigens. Immunogenic or antigenic compositions comprising the proteins are useful as vaccines and also in compositions comprising the proteins are useful as vaccines and also in conditions. The sequences are useful for the detection or diagnostic assays The sequences are useful for the detection or characteristic of S. pneumoniae infection, by contacting a sample to be tested composition or expression of the protein or polypeptide are useful in the function or expression of the protein or polypeptide are useful in compositions in the treatment or prophylaxis of S. pneumoniae infection, as the sequences can be used to treat S. pneumoniae infection, they can be used to treat bacterial pneumonia, which has high rates in conjugation of the protein of the proteins with predisposing conditions can be applied to treat bacterial pneumonia, which has high rates in conjugation of the composition of the protein of the proteins with predisposing conditions can be used to treat bacterial pneumonia, which has high rates in composition of the protein of the prot
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                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 37; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcal treatment and
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19-MAR-1999;
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                         85.7%;
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Score 24; DB 21; L
Pred: No. 5.8e+02;
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Maximum DB
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
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6: /cgn2_6/ptodata/2,
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Match
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28
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/cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
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US-09-085-305-9
US-08-08-986-2
US-08-08-717-312-2
US-08-717-312-2
US-08-717-312-2
US-08-64-08-2
PCT-US94-07886-2
US-09-138-614-25
US-09-138-935-6
US-09-08-9315-793-12
US-08-711-602D-46
US-08-711-602D-46
US-08-953-041-2
US-09-08-943-521-6
US-08-08-121-714-6
US-08-477-114-6
US-08-477-114-6
US-08-477-112-6
PCT-US93-0832-6
US-08-315-461-7
US-08-9315-461-7
US-08-9315-461-7
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US-08-205-018-2
US-08-395-580-2
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AL TGUMENTS	US-09-257-490-13	US-08-860-519-12	US-08-466-662-6	US-08-471-491-6	US-08-470-260-6	US-08-466-248-30	US-08-432-697-30	US-08-467-822-30	US-08-472-240A-16	US-08-889-841B-5	US-08-889-841B-2	US-08-889-841B-16	US-08-889-841B-12	US-08-889-841B-10	US-08-889-841B-8	US-09-026-408-3	US-09-348-817A-4	US-08-840-204-2	
	Sequence 13, Appl	Sequence 12, Appl	Sequence 6, Appli	Sequence 6, Appli	Sequence 6, Appli	Sequence 30, Appl	Sequence 30, Appl	Sequence 30, Appl	Sequence 16, Appl	Sequence 5, Appli	Sequence 2, Appli	Sequence 16, Appl	Sequence 12, Appl		Sequence 8, Appli	Sequence 3, Appli	Sequence 4, Appli	Sequence 2, Appli	

## GENERAL INFORMATION: APPLICANT: LAW, MATCUS D APPLICANT: Dietz, Jon M TITLE OF INVENTION: Use of Translationally altered RNA to TITLE OF INVENTION: Confer Resistance to Maize Dwarf Mosaic V TITLE OF INVENTION: Monocotyledonous Plant Viruses NUMBER OF SEQUENCES: 8 CORRESPONDENCE ADDRESS: ADDRESSEE: CIBA-Geigy Corporation STREET: 7 Skyline Drive CITY: Hawthorne STATE: NY ; MOLECULE TYPE: US-08-496-944-2 ATTORNEY/AGENT INFORMATION: NAME: Elmer, James Scott REGISTRATION NUMBER: 36,129 REFERENCE/DOCKET NUMBER: CGC INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 2763 amino acids TYPE: amino acid Sequence 2 Patent No. Matches Query Match Best Local ZIP: 10532 COMPUTER READBLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS\_MS-DOS SOFTWARE: PatentID Release #1.0, V CURRENT APPLICATION DATA: 1 EEIIMR 6 |||:|| 2064 EEIVMR 2069 APPLICATION NUMBER: US/08/496,944 FILING DATE: CLASSIFICATION: 435 TYPE: amino acid TOPOLOGY: linear COUNTRY: 2, Application 5. 6040496 Similarity 5; Conserv USA Conservative protein 96.4%; US/08496944 Release #1.0, Version 1; CGC 1814 Score 27; DB 3; Pred. No. 3.3e+02 Mismatches Maize Dwarf Mosaic Virus and Other #1.30B 0 Length 2763; 0; Gaps . 0

it No.

2, Application US/08205018

INFORMATION:

Reddy, Usharani R.

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; MOLECULE TYPE: protein US-08-205-018-2
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Best Local :
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SEQUENCE CHARACTERISTICS:
LENGTH: 668 amin
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MEDIUM TYPE: Floppy
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REFERENCE/DOCKET NUMBER: CH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
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                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
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| 409 EELVMR 414
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ATTORNEY/AGENT INFORMATION
                                                                                                                                                                           CORRESPONDENCE ADDRESS
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COMPUTER: IBM PC COMPUTER: DC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn_Release #1.0, Version #1.25
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CTTY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/205,018 FILING DATE:
                                                                                                                                                                                                         PPLICANT: Usharani R. Reddy, David Pleasure and the Children's PPLICANT: Hospital of Philadelphia Protein Kinase, Nucleic Acid TILE OF INVENTION: Sequences Encoding the Same and Methods Relations of Invention:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
les 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Gaumond, Rebecca
REGISTRATION NUMBER: 3
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                                                                                                       STREET: One L-CITY: Philadelphia
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COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                           DDRESSEE:
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5. 5676945
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                                                                                     U.S.A.
                                   inch disk, 720 Kb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89.3%; Score 25; 66.7%; Pred. No. 2
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uences Encoding the Same and Methods Related Thereto
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; MOLECULE TYPE: protein US-08-395-580-2
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PCT-US95-02792-2
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TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/2 FILING DATE: 01-MAR-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
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                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/2)
FILING DATE: 01-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                          SOFTWARE: WordPerfect CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
SEQUENCE CHARACTERISTICS:
LENGTH: 859 amino acid
                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Usharani R. Reddy, David Pleasure and the Children's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   409 EELVMR 414
                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPEFFACT 6 1
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                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Rebecca L. Ralph
REGISTRATION NUMBER: 3
                                                                                                     NAME: Rebecca L. Ralph REGISTRATION NUMBER: 35 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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                                                                   CELEPHONE:
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amino acid
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One Liberty Place - 46th Floor
   859 amino acids
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Sequences Encoding the Same and Methods Related Thereto
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Pred. No.
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; MOLECULE TYPE: PCT-US95-02792-2

protein

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RESULT 6
US-08-089-986-2
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Patent No. 6191269
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Francis, Carol L
REGISTRATION NUMBER: 36,513
REFERENCE/DOCKET NUMBER: 6510
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Pollock, Allan
APPLICANT: Lovett, David H.
APPLICANT: Turck, Johanna
TITLE OF INVENTION: Selective Induction of Apoptosis in
TITLE OF INVENTION: Malignant Cancer Cells by Delivery of N-Terminal
TITLE OF INVENTION: Interleukin-1-Alpha Pro-Piece Polypeptide
NUMBER OF SEQUENCES: 30
                                                                                                                                                                                                                         MOLECULE TYPE: No. 6191269e
                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 265 amino acid
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PRIOR APPLICATION NUMBER:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Bozicevic & Reed, LLP
STREET: 285 Hamilton Ave, Suite 200
                                                              101 EEVIMK 106
                                                                                                                                                                                                                                     TYPE: amino a STRANDEDNESS: TOPOLOGY: lin
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OPERATING SYSTEM: DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: CA
                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 650-327-3231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/085,305 FILING DATE: 29-MAY-1998
                                                                                            1 EEIIMR 6
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amino acid
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Pred. No. 3.1e
2; Mismatches
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Pred. No. 1.7e+02
                                                                                                                              Mismatches
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1e+02;
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Patent No
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Best Local :
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE: 306 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Egolf, Christopher
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 720:
TELEPOMUNICATION INFORMATION:
TELEPOMUNICATION TO TELEPOMORE: 215-757-1590
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                        equence 2, Application US/08478585
etent No. 5650308
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Bacillus thuringlensis Transposon Th5401
TITLE OF INVENTION: and Its Use in a Site-Specific Recombination System For TITLE OF INVENTION: Recombinant Bacillus thuringlensis Strain Development
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CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: and Its Use in a Site-Specific Recombination System For TITLE OF INVENTION: Recombinant Bacillus thuringiensis Strain Development
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  172 EDVIMR 177
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TOPOLOGY: linear
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                 ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S ADDRESSEE: Nadel
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Philadelphia
Pennsylvania
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Philadelphia
Pennsylvania
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Pred. No. 2e+02;
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, MOLECULE TYPE: protein US-08-478-585-2
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                                                                                                                                                                                                     FILING DATE: 20-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/266,408
FILING DATE: 24-JUL-1994
APPLICATION UNMBER: US 08/089,986
EPILING DATE: 08-JUL-1993
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
Query Match

Best Local Similarity bo.,

Chaq 4; Conservative
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Best Local Similarity
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APPLICATION NUMBER: US 08/089

FILING DATE: 08-JUL-193

ATTORNEY/AGENT INFORMATION:

NAME: EGOLF CIN-1stopher

REGISTRATION NUMBER: 27633

REFERENCE/DOCKET NUMBER: 7205

TELECOMUNICATION INFORMATION:

TELECOMUNICATION INFORMATION:

TELEPHONE: 215-757-1590
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acids
TYPE: amino acid
TOPOLOGY: liner
                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IITLE OF INVENTION: Bacillus thuringiensis Transposon Tn5401
IITLE OF INVENTION: and Its Use in a Site-Specific Recombination System For INTEL OF INVENTION: Recombinant Bacillus thuringiensis Strain Development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        172 EDVIMR 177
                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                    TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSEE: Panitch Schwarze Jacobs & Nadel c/o A.S. Nadel
T: 1601 Market Street, 36th Floor
Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pennsylvania
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                                                                                                                                                          linear
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                                       85.7%;
66.7%;
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                           Score 24; DB
Pred. No. 2e+0
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 24; DB 1; Length 306;
Pred. No. 2e+02;
2; Mismatches 0; Indels
                                           DB 1;
2e+02;
                                                              Length 306;
                           0; Indels
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PCT-US94-07886-2
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                                                                                                                                                                                                                                                                                        Sequence 2, Application PC/TUS9407886 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,986
FILING DATE: 08-JUL-1993
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                    APPLICANT: Baum, James A.
TITLE OF INVENTION: Beilus thuringiensis Transposon Tn5401
TITLE OF INVENTION: and Its Use in a Site-Specific Recombination System For TITLE OF INVENTION: Recombinant Bacillus thuringiensis Strain Development NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
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TITLE OF INVENTION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172
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STREET: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
                                                                                        STATE: Pennsylvania
COUNTRY: U.S.A.
                                                                                                                                 CITY: Philadelphia
                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EEIIMR 6
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'E: Pennsylvania
TTRY: U.S.A.
19103
                                                                          19103
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                                                                                                                                                E: Panitch Schwarze Jacobs & Nadel c/o A.S. Nadel 1601 Market Street, 36th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and Its Use
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Pred. No. 2e+02;
2; Mismatches
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US-08-687-916-25; A
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APPLICATION NUMBER: US 08/089,986
FILING DATE: 08-JUL-1993
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 306 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local Similarity
                                                                                                                                                     CLASSIFICATION: 800

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/391,000

FILING DATE: 21-FEB-1995

ATTORNEY/AGENT INFORMATION:
NAME: Dadio, Susan M.
REGISTRATION NUMBER: 40,373

REFERENCE/DOCKET NUMBER: 028750-138

TELECOMMUNICATION INFORMATION:
                                                                                 TELEFAX: (703) 836-2021
NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                        OFFINARE: PATEULA:
SOFTWARE: PATEULA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U5/08/687,916
APPLICATION NUMBER: 29-JUL-1996
FILING DATE: 29-JUL-1996
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 EDVIMR 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ITLE OF INVENTION:
ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: BURNS, DOA
STREET: P.O. Box 1404
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                STRANDEDNESS:
                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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                                                                   ENGTH:
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                                             amino acid
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                                                                                                                                                                                                                                                                                                                                                                                PatentIn Release #1.0, Version #1.30
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                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESS
                                                                                                                                           703) 836-6620
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                          single
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RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE
SUBURIT N-METHYLTRANSFERASE AND METHOD OF INACTIVATING
RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE
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                                                                                                        25:
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Pred. No. 2e+02;
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-138-614-25
                               US-09-315-793-12
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                                                                                                                                                        Query Match
Best Local S
Matches 4
Sequence 12, Application US/09315793 Patent No. 6221597
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Matches
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Best Local
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0,
                                                                                          1 EEIIMR 6
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196 EEVILR 201
                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 490 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/687,916
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                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                               NAME: Dadio, Susan M. REGISTRATION NUMBER: 40,373
REFERENCE/DOCKET NUMBER: 03
LECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: United States ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE
                                                                                                                                                                                                                                                                                                                                                    MATION FOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25,
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amino acid
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4; Conservative
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OR SEQ ID NO: 25:
                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                  single
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ISOLATE SPINACH

ISOLATE SPINACH

RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE

SUBUNIT N-METHYLTRANSFERASE AND METHOD OF INACTIVATING

RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOANE,
                                                                                                                                                                        85.7%;
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                                                                                                                                                        Score 24; DB 4;
Pred. No. 3.1e+02;
2; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                028750-138
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Pred. No. 3.1e+02;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Version #1.30
                                                                                                                                                                                      Length 490;
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GENERAL INFORMATION: APPLICANT: Roberts, Christopher J

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US-08-781-020-6
US-08-781-020-6
Sequence 6, Application US/08781020
Patent No. 5792749
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 1698
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-315-793-12
                  Ş
                                                                                                                                                                ; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-781-020-6
                                                          Ouery Match

92.1%; Score 23; DB I;

Best Local Similarity 100.0%; Pred. No. 39;

Matches 5; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 85.7%;
Best Local Similarity 83.3%;
Matches 5; Conservative
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CURRENT FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: ESSENTIAL GENES OF YEAST AS TARGETS FOR ANTIFUNGAL TITLE OF INVENTION: AGENTS, HERBICIDES, INSECTICIDES AND ANTI-PROLIFERATION TITLE OF INVENTION: DRUGS
                                                                                                                                                                                                                                                                  TELEFAX: 703-391-9035
NFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/781,020
FILING DATE: 09-TAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Whitham, Michael E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          494 EEIIVR 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Reston
STATE: VA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ITLE OF INVENTION: METHOD AND COMPOSITION FOR LOWERING LOW ITLE OF INVENTION: DENSITY LIPOPROTEIN CHOLESTEROL
1 EEIIM 5
                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                      NAME: Whitham, Michael E. REGISTRATION NUMBER: 32,635
REFERENCE/DOCKET NUMBER: VCU-16
LECOMMUNICATION INFORMATION:
TELEPHONE: 703-391-2510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Reston In:
STREET: Suite 900
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; SEQ ID NO 6; LENGTH; 33; TYPE: PRT; ORGANISM: Homo sapiens US-09-038-935-6
Search completed: March 18, 2002, 09:49:42
Job time: 226 sec
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Best Local Similarity
Thes 5; Conserv
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CURRENT FILING DATE: 1998-03-12
EARLIER APPLICATION NUMBER: 08/781,020
EARLIER FILING DATE: 1997-01-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-038-935-6
                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.0
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ITLE OF INVENTION: METHOD AND COMPOSITION FOR LOWERING LOW DENSITY
ITLE OF INVENTION: LIPOPROTEIN CHOLESTEROL
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PPLICANT: Janciauskiene,
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Maximum Match 100%
Listing first 45 summaries
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R;Kwon, Y.T.; Reiss, Y.; Fried, V.A.; Hershko, A.; Yoon, J.K.; Gonda, D.K.; Sangan, Proc. Natl. Acad. Sci. U.S.A. 95, 7898-7903, 1998
A;Title: The mouse and human genes encoding the recognition component of the N-end A;Reference number: Z17977; MUID:98318583
A;Accession: T14318
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A;Molecule type: mRNA
A;Residues: 1-1757 <KWO>
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N;Alternate names: N-recognin E3-alpha
C;Species: Mus musculus (house mouse)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
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## ALIGNMENTS

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conserved hypothetical protein MTH1148 - Methanobacterium thermoautotrophicum (strai c; Species: Methanobacterium thermoautotrophicum C; Species: Methanobacterium thermoautotrophicum C; Dete: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999 C; Accession: H69019 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999 C; Accession: H69019 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999 C; Accession: H59019 #sequence not shown; Times Name Complete General Procession: Mail Not Name Complete General Procession: Methanobacterium thermoautotrophicum Delta H: faraccession: H69019 #MID:98037514 A; Accession: H69019 #MID:98037514 A; Accession: H69019 #tree-name sequence acid sequence not shown; translation not shown A; Status: preliminary: nucleic acid sequence not shown; translation not shown
A;Cross-references: GB:AE000884; GB:AE000666; NID:g2622242; PIDN:AAB85637.1; PID:g26A;Experimental source: strain Delta H
C;Genetics:
                                                                                             A; Molecule type: DNA
A; Residues: 1-157 < MTH>
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Best Local Similarity
Matches 5; Conserv
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Pred. No. 2.8e+02;
1; Mismatches (
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hypothetical protein - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
C;Species: Synechocystis sp.
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C;Accession: S76994
C;Accession: S769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          anthranilate synthase component I XF1914 (imported) - Xylella fastidiosa (strain C;Species: Xylella fastidiosa C;Date: 18-Aug-2000 *sequence_revision 20-Aug-2000 *text_change 02-Sep-2000
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R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
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Matches 5
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Molecule type: DNA
Residues: 1-263 <KRAN>
Cross-references: EMBL:D64005; GB:AB001339; NID:g1001779; PIDN:BAA10686.1; PID:d101133;
Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reference number: S74322; MUID:97061201
Accession: S76994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title: The genome sequence of the plant pathogen Xylella fastidiosa. Reference number: A82515; MUID:20365717; Reference number A59328 below: Note: for a complete list of authors see reference number A59328 below
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Superfamily: anthranilate synthase component I
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Local Similarity 83.3%;
les 5; Conservative
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Pred. No.
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C;Superfamily: Pyrococcus
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5; Conserve
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A; Residues: 1-886 <BRO>
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A; Accession: S48371
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submitted to the EMBL
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A; Map position: 9L
C; Superfamily: Saccharomyces cerevisiae hypothetical protein YIL073c
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superoxide dismutase (EC 1.15.1.1) (Fe) -
C; Species: Legionella pneumophila
                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-149 <KAW>
A;Residues: 1-149 <KAW>
A;Cross-references: GB:AJZ48288; GB:AL096836; NID:g5458960; PIDN:CAB50448.1; PID:g54:
A;Experimental source: strain Orsay
                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Description: Pyrococcus
A; Reference number: A75001
A; Accession: B75001
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A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein PAB1019 · Pyrococcus abyssi (strain Orsay) C;Species: Pyrococcus abyssi C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change
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Pred. No. 2.4e+02;
1; Mismatches 0
                                                                                                                                                                                           Score 25; DB
Pred. No. 64;
1; Mismatches
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1.3e+02;
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                       Legionella pneumophila
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probable UDP-N-acetyl-D-mannosaminuronic acid transferase - Escherichia coli N;Alternate names: hypothetical protein o246 C;Species: Escherichia coli C;Species: Escherichia coli C;Date: 12-Sep-1997 *sequence_revision 17-Sep-1997 *text_change 08-Oct-1999 C;Date: 12-Sep-1997 soquence_revision 17-Sep-1997 *text_change 08-Oct-1999 C;Accession: G65183; S30688
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C;Reywords: iron; metalloprotein; oxidoreductase
F;27,74,157,161/Binding site: iron (His, His, Asp,
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A; Reference number: JS0749
A; Accession: JS0749
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A;Experimental source: strain Philadelphia-1
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A; Residues: 1-192 < AME>
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A;Title: The complete genome sequence of Escherichia
A;Reference number: A64720; MUID:97426617
A;Accession: G65183
C; Accession:
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                                                                                                                              ATP binding
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A; Residues: 1-119, 'AV',122-177,'X',179-246 <DAN>
A; Residues: 1-119, 'AV',122-177,'X',179-246 <DAN>
A; Cross-references: EMBL:M87049; NID:9836656; PIDN:AAA67594.1;
A; Note: the nucleotide sequence was submitted to the EMBL Data
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A;Residues: 1-246 <B
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                                   Reference number: S30660; MUID:92358234
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;Accession: JS0749
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Pred. No. 1.1e
1; Mismatches
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Pred. No. 84;
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1.1e+02;
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Library, November 1992
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A;Molecule type: DNA
A;Residues: 1-287 <KAW>
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5; Conserv
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A;Title: A DNA-polymerase-related reading frame (pol-r)
A;Reference number: S39814; MUID:94363738
A;Accession: S39814
A;Molecule type: DNA
A;Residues: 1-289 <-DOH>
A;Cross-references: EMBL:X74132; NID:9439279; PIDN:CAA5:
A;Experimental source: strain Haio; etiolated shoots
C;Genetics:
A;Gene: pol-r
A;Gene: pol-r
A;Gene: mitochondrion
C;Keywords: mitochondrion
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A;Cross-references: EMBL:L11577; NID:g310629; PID:g310631 A;Experimental source: strain PK488 C;Superfamily: short-chain ARP-binding cassette proteins; F;29-221/Domain: ATP-binding cassette homology <ABC>
                                                                                                                                                                                                                                     DNA polymerase homolog pol-r - rye mitochondrion (strain C;Species: mitochondrion Secale Cereale (Tye) A;Variety: strain Halo C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_C;Accession: S39814 R;Dohmen, G: Tudzynski, P. R;Dohmen, G: Tudzynski, P. Curr Genet. 25, 59-65, 1994
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R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
submitted to the EMBL Data Jibrary, July 1999
A;Description: Pyrococcus abyssi genome sequence:
A;Reference number: A75001
A;Accession: E75202
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875202
Gipeptide abc transporter, dipeptide-binding protein PAB0093 - Pyrococcus abyssi
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
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Infect. Immun. 62, 4469-4480, 1994
A;Title: Nucleotide sequence of the Streptococcus gordonii PK488 coaggregation adhes A;Reference number: 217283; MUID:95012638
A;Recession: T11549
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lip1d A biosynthesis lauroyl acyltransferase VCO213 [imported] - Vibrio cholerae (strain ;Species: Vibrio cholerae (strain c;Species: Vibrio cholerae C;Date: 18-Aug-2000 *sequence_revision 20-Aug-2000 *text_change 02-Feb-2001 C;Accession: G82350
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Curr. Genet. 25, 59-65, 1994
A;Title: A DNA-polymerase-related reading
A;Reference number: S39814; MUID:94363738
A;Accession: S39823
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A;Residues: 1-318 <HEI>
A;Cross-references: GB.AE004111; GB:AE003852; NID:99654614; PIDN:AAF93389.1;
A;Experimental source: serogroup O1; strain N16961; biotype E1 Tor
                                                                                                                                                                                                                                                                                                       A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A;Reference number: A82035; MUID:20406833 A;Accession: G82350
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Nature 405, 477-483, 2000
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A;Experimental source: strain B-P2; etiolated shoots
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, Ju
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R;Dohmen, G.; Tuo
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Genome: mitochondrion
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1 EEIIMR 6
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5; Conservative
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Pred. No. 1.4e+02;
1; Mismatches (
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Pred. No. 1.4e+02;
1; Mismatches 0;
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Pred. No. 1.3e+02;
1; Mismatches 0
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H.; Dragoi, I.; Sellers,
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C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; c;Keywords: ATP; leucine zipper; nucleotide binding; P-loop; phosph F;123-371/Domain protein kinase homology KKIN>
E;131-139/Region: protein kinase ATP-binding motif F;443-471/Region: leucine zipper motif F;443-471/Region: nucleotide-binding motif F;538-545/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:U07358
A;Experimental source: brain
A;Experimental source: brain
A;Note: the nucleotide sequence for this amino acid sequence is inconsistent with th
he codon ACC for residue 661 as Pro, the codon GAACCACCTCCTCA for residues 664-668
C;Comment: This protein belongs to the family of non-receptor kinase.
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Blochem. Blophys. Res. Commun. 202, 613-620, 1994
Blochem. Blophys. Res. Commun. 202, 613-620, 1994
A;Ttle: Cloning of a novel purative protein kinase having
A;Reference number: JC2363; MUID:94311945
A;Accession: JC2363
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A;Cross-references: GDB:383963; OMIM:600447
A;Map position: 12q13-12q13
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A; Residues: 1-668 < RED>
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R;Deckert, G.; Warren, P.V.;
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C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 21-Jan-2000
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DT 20-AUG-2001 (Rel. 40, Last annotation update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DT 20-BUG-2001 (Rel. 31, Created)
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	P05121 homo sapien	-	-	-	029715 archaeoglob	-	٠.	_	~	P46245 buchnera ap	-	Q58087 methanococc	

RESULT 2 SODF_LEGPN STANDARD; PRT; 192 AA. ID SODF_LEGPN STANDARD; PRT; 192 AA. AC p31108; DT 01-JUL-1993 (Rel. 26, Created) DT 01-JUL-1993 (Rel. 26, Last sequence update) DT 30-MAY-2000 (Rel. 39, Last annotation update)	Query Match 92.9%; Score 26; DB 1; Length 886; Best Local Similarity 83.3%; Pred. No. 86; Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0; Qy 1 EEIIMR 6	SWISS-PROT entry is copyright een the Swiss Institute of Bi European Bioinformatics Instit by non-profit institutions fied and this statement is not ties requires a license agreement an email to license@isb-siend an	OC Saccharomycetales; Saccharomycetaceae; Saccharomycets.  OX NCBL_TaxID-4932; RN [1] RN [2] RN [2] RN [3] RN [4]

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"Cloning and nucleotide sequences of iron and copper-zinc su
dismutase genes of Legionella pneumophila and their distribu
among Legionella species.";

Jpn. J. Med. Sci. Biol. 49:167-186(1996).

-- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED
-- CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS.

-- CATALYTIC ACCIVITY: 2 PEROXIDE RADICAL + 2 H(+) = O(2) +
-- SUBUNIT: HOMODIMER.
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SEQUENCE
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SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE-92358234; PubMed-1379743;
MEDLINE-92358234; PubMed-1379743;
Maniels D.L., Plunkett G. III, Burland V.D., E
"Analysis of the Escherichia coli genome: DNA
from 84.5 to 86.5 minutes.";
                                                                                                                                                                                                                                                                                                                                                                                    01.AUG-1992 (Rel. 23, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROBABLE UDP-N-ACETYL-D-MANNOSAMINURONIC ACID
(UDP-MANNACA TRANSFERASE).
WECG OR RFFM OR B3794.
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Escherichia.
                                                                                                                                                                                                                                                                                                                                                         Escherichia coli
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aceae; Legionella
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                                      Blattner F.R.;
A sequence of the
                                                                                                                                                                                                                                                                                                                      Enterobacteriaceae;
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P42360;
01-NOV-1995 (;
01-NOV-1995 (;
01-OCT-1996 (;
HYPOTHETICAL
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CONFLICT 120 121 VL -> AV (IN REF. 1).
SEQUENCE 246 AA; 27928 MW: 0D9435DBA6*60~~~
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                                                                                                                                                                                                                        Streptococcus gordoni: Bacteria; Firmicutes; Streptococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRGC
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Science 277:1453-1474(1997).
-I- PATHWAY: INVOLVED IN THE SYNTHESIS OF ENTEROBACTERIAL COMMON ANTIGEN (ECA) AND REQUIRED FOR SYNTHESIS OF LIPOPOLYSACCHARIE O-SIDE CHAINS.
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MEDLINE-97426617; PubMed-9278503;
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                                                                                                                                                                                                                                                                                                                            MEDLINE-95012638; PubMed-7927711;
Kolenbrander P.E., Andersen R.N.,
                                                                                                                                                                                                                                                                                                                                                                              STRAIN-PK488;
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=29390;
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(Rel. 32, Last sequence update)
(Rel. 34, Last annotation update)
L ABC TRANSPORTER ATP-BINDING PROTEIN
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Pred. No. 40;
1; Mismatches
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MEDLINE-93021519; PubMed-7935620;

IIVINE MINIME T, Prince A.M., Lustigman S.;

IIVINE M. Hulma T, Prince A.M., Lustigman S.;

*Identification and characterization of an Onchocerca volvulus c
clone encoding a highly immunogenic calponin-like protein.";

MOI. Biochem. Parasitol. 65:135-146(1994).

-!- FUNCTION: COULD BE INVOLVED IN MUSCLE CONTRACTION.

-!- TISSUE SPECIFICITY: FOUND IN THE LONGITUDINAL MUSCLES BELOW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003593; AAA.
InterPro; IPR003499; ABC_transportr.
InterPro; IPR001647; ATP_CTP_A.
InterPro; IPR001667; ATP_CTP_A.
SMART; SM0382; AAA; 1.
SMART; SM0382; AAA; 1.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
BYPOTENTIAL)
SEQUENCE 251 AA; 28054 MW; AED59C66F677D031 CRC64;
                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Onchocercidae, Onchocerca.
NCBI_TaxID-6282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Onchocerca volvulus.
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CALPONIN HOMOLOG OV9M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1994 (Rel.
01-FEB-1996 (Rel.
01-FEB-1996 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L11577; AAA71945.1; -.
                                                                  REPEAT
REPEAT
REPEAT
                                                                                                                                                   Pfam; PF
PROSITE;
                                                                                                                                                                                                                                                                                                                          -1- DEVELOPMENTAL STAGE: PRESENT IN INFECTIVE LARVAE AND ADULT STAGES.
1- MISCELLANEOUS: THERE ARE APRANTLY SEVERAL FORMS OF THE NATIVE
PROTEIN WHICH APPEAR TO BE EXPRESSED IN A STAGE-SPECIFIC MANNER.
-1- SIMILARITY: BELONGS TO THE CALPONIN FAMILY
-1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-22 IS THE INITIATOR.
                                                                                                                                                                                             EMBL; U01099; AAA20215.1; ALT_SEQ
                                                        SEQUENCE
                                                                                                              REPEAT
                                                                                                                                                                                  nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 EEIIMK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 83.
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                                                                                                                                                                   IPR000557; Calponin_repeat.
0402; calponin; 7.
                                                      98
151
197
244
285
378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                 123
176
222
269
310
41852
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                                                                                                                                                      CALPONIN;
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   68
                                                        M.
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1; Mismatches
                                                    CALPONIN-LIKE 26 AA N
                                                                                                                                                      5
   Score
Pred.
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   No.
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   DB
63;
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                                                                                                                                                                                                                                                          RESULT 7
NCPR_MUSDO
ID NCPR_MUSDO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-AUG-2001
20-AUG-2001
20-AUG-2001
                                  007994;
01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
01-0CT-1994 (Rel. 30, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
NADPH-CYTOCHROME 9450 REDUCTASE (EC 1.6.2.4) (CPR) (P450R).
Musca domestica (House fly)
Musca domestica (House fly)
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF02483; SMC_C; 1.

Pfam; PF02483; SMC_C; 1.

DNA repair; ATP-binding; Complete proteome.

ATP (POTENTIAL).

NP_BIND 29 36 ATP (POTENTIAL).

NP_BIND 29 36 ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE000695; AAC06789.1; ... InterPro; IPR003493; ABC_LIANSPORTI. InterPro; IPR003405; SMC_C. Pfam; PF02483; SMC_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-98196666; PubMed-9537320; Deckert G., Warren P.V., Gaasterland T., Young W.G., Ler Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay Neldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA REPAIR PROTEIN RECN OR AQ_561.
Aquifex aeolicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RECN_AQUAE
066834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 392:353-358(1998).
-I FUNCTION: MAY BE INVOLVED IN RECOMBINATIONAL DNA (BY SIMILARITY).
-I- SIMILARITY: BELONGS TO THE RECN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Aquificales;
NCBI_TaxID=63363;
                NCBI_TaxID-7370;
                                                                                                                                                                                                                                                                                                                                                                                                          . 1 EEIIMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88
                                                                                                                                                                                                                                                                                                                                                                                66 EEIILR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 83. 5; Conservative
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40, Last
40, Last
10, RECN (RE
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83.3%;
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ast annotation update)
(RECOMBINATION PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 25; DB
Pred. No. 88;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
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                                                                     Brachycera; Muscomorpha;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a collaboration
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PYROPHOSPHATE

ENDOGENOUS

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Query Match
Best Local S
Matches 4
HSR_CAVPO STANDARU;

HSR_CAVPO STANDARU;

P70106;

P70106;

01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEAT-STABLE ENTEROTOXIN RECEPTOR PRECURSOR (GC-C) (INTESTINAL GUANYLATE CYCLASE) (EC 4.6.1.2) (STA RECEPTOR) (GUANYLYL CYCLASE C).
GUCY2C OR GUC2C.
Cavia porcellus (Guinea pig).
Tharvota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Tharvota; Metazoa; Chordata; Hystricognathi; Cavidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Membrane.

NP_BIND

NP_BIND

NP_BIND

NP_BIND

NP_BIND
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HSSP: P00388; IAMO.
InterPro; IPR003097; FAD_binding.
InterPro; IPR001094; Flavdxn-like.
InterPro; IPR001709; Flavpyrid_cyt_redctse.
InterPro; IPR0017433; Oxidored_FAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00667; FAD_binding; 1.
Pfam; PF00175; oxidored_fad; 1
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STRAIN-RUTGERS; TISSUE-Abdomen;
MEDLINE-93284260; PubMed-850818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EEIIMR 6
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4; Conserv
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671 /
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Carino F.A., Feyereisen R.;
d deduced protein sequence of house fly NADPH-cytochrome
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322
458
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634
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Pred. No. 1.2e+02;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FMN (PYRIMIDINE PART) (BY SIMILARITY).
FAD (ADP PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
A00A2C35DFDBD129 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FMN; FAD; NADP; Endoplasmic reticulum;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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Best Local S
Matches 5
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SEQUENCE
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CARBOHYD
CARBOHYD
      ELYS_HALKA STANDARD; PRT; 154 AA Q01382; Q1-APR-1993 (Rel. 25, Created) Q1-APR-1993 (Rel. 25, Last sequence update) Q1-FEB-1995 (Rel. 31, Last annotation update) EGG-LYSIN PRECURSOR (SPERM-LYSIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001828; ANP_receptor.
InterPro; IPR0010719; Euk_pkinase.
InterPro; IPR001054; Guanytt_cyclase.
Pfam; PP01094; ANP_receptor; 1.
Pfam; PP00211; guanylate_cyc; 1.
Pfam; PP00059; pkinase; 2.
SMART; SM00044; CYCC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                          HALKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Z74734; CAA98989.1; -. HSSP; Q02846; 1AWL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kruhoeffer M., Cetin Y., Kaempf U., Forssmann M.-G.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
-I-FUNCTION: RECEPTOR FOR THE E.COLI HEAT-STABLE ENTEROTOXIN (E.COLI ENTEROTOXIN MARKEDLY STIMULATES THE ACCUMULATION OF CGMP IN MARMALIAN CELLS EXPRESSING GC-C). ALSO ACTIVATED BY THE ENDOGENOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00452; GUANYLATE_CYCLASES_1; PS50125; GUANYLATE_CYCLASES_2; PROSITE; PS50011; PROTEIN_KINASE_DOM; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Colon;
                                                                                                                                                                                                                                                                                                          674
                                                                                                                                                                                                                                                                                                                                        1 EEIIMR 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEPTIDE GUANYLIN.

CATALITIC ACTIVITY: GTP = 3, '5'-CYCLIC GMP +
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN
SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: CONTAINS 1 PROTEIN KINASE-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                          QEIIMR
                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          434
458
492
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                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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24 43

34 457

4 57

5 7 957

7 957

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1 287

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC...)
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 25; DB
Pred. No. 1.9e
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GUANYLATE CYCLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTEIN KINASE-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HEAT-STABLE ENTEROTOXIN RECEPTOR
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-:

RESULT HSER\_C/

В δÃ

DB 1; L. 1.9e+02; 0;

Length 1076;

CRC64;

(POTENTIAL)

(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
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Indels

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Gaps

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RESULT 10
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RP SEQUENCE FROM N.A.

RR SETABLEGER A.F., STRAUBINGER R.K.;
RS SETABLEGER A.F., STRAUBINGER R.K.;
RS SUBMILLEGE (FEBS-1998) to the EMBL/GenBank/DDBJ databases.

RL Submitled (FEBS-1998) to the EMBL/GenBank/DDBJ databases.

RL SUBMITLEGER (FEBS-1998) TO THE TABLEAGE B. B-CELL

CC -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES

CC HATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.

CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING

CC IDENTIFIED AS ENDOGROUS PROGENS, AND ARE REPORTED TO STIMULATE

CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.

CC GEN SIMILARITY).

CC -!- SUGUNIT: MONOMER (BY SIMILARITY).

CC -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE

AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.

CC -!- MIGGELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SERMENT IN THE

CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                 046612;
15-DEC-1998
15-DEC-1998
15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          by positive Darwinian selection.";
Biol. Bull. 182:97-104(1992).

FUNCTION: DISSOLVES THE EGG VITELLINE LAYER NONENZYMATICALLY
FUNCTION: DISSOLVES THE EGG VITELLINE OF ABOUT 3 MU-M IN
DIRING FERTILIZATION. IT CREATES A HOLE OF ABOUT 3 MU-M IN
DIAMETER THROUGH WHICH THE SPERM PASS.

-1- SUBURIT: HOMODIMER.
-1- TISSUE SPECIFICITY: SPERM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haliotis kamtschatkana (Pinto
Eukaryota; Metazoa; Mollusca;
Haliotidae; Haliotis.
                                                                                                                                                                                                                                                                                 LILA.
Canis familiaris (Dog).
Canis familiaris (Dog).
Eukaryota, Metazoa, Chordata, Craniata, Ver
wammalia; Eutheria; Carnivora, Fissipedia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001379; Egg_lysin. Pfam; PF01303; Egg_lysin; 1. ProDom; PD002750; Egg_lysin; 1. Fertilization; Sperm; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M59970; AAA29200.1; -. HSSP; P04552; 1LYN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=6457;
                                                                                                                                                                                                                                                                             NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  IL1A_CANFA
                                                                                                                                                                                                                                                                                                                                                                  NTERLEUKIN-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EEIIMR
||||:|
39 EEIIVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y.H., Vacquier V.D.;
divergence of species-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 83. 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
                                                                                                                                                                                                                                                                                                                                                              (Rel. 37, Created)
(Rel. 37, Last sequence update)
(Rel. 37, Last annotation update)
-1 ALPHA PRECURSOR (IL-1 ALPHA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                 37, Created)37, Last sequence up37, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18386 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85.7%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 24;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGG-LYSIN.
; 8875D2B9E6CF3564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           abalone).
Gastropoda; Archaeogastropoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       abalone sperm lysins is promoted
                                                                                                                                                                                                                                                                                                                                                                                                                                                        265
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43;
                                                                                                                                                                                                                                                                                                Vertebrata;
ia; Canidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRC64;
                                                                                                                                                                                                                                                                                                  Euteleostomi;
Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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RESULT 11

ARCC_HELPY
ID ARCC_YELPY
ID ARCC_YELPY
AC P5612;
DT 01-NOV-1997
DT 01-NOV-1997
DT 20-AUG-2001
DE CHORISMATE;
DE PHOSPHOLYAS;
GN ARCC OR HPO
OS Helicobacte;
OC NCBL_TAXID=
RN SEQUENCE FR
RN SUJENCE FR
RN LIFTUS B.,
RA LIFTUS B.,
RA LIFTUS B.,
RA HAYES W.S.,
RA HAYES W.S.,
RA COTCON M.D.,
RA COTCON M.D.,
RA COTCON M.D.,
RA HAYES W.S.,
RA PERFORMAN
COTORISM
CC -1- COPACTO
CC -1- COPACTO
CC -1- COPACTO
CC -1- SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SO TITE
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Best Local S
Matches 4
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01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CHORISMATE SYNTHASE (EC 4.6.1.4) (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE
PHOSPHOLYASE).
AROC OR HP0663.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF047011; AAC03066.1;
InterPro; IPR000975; Interleukin_1.
InterPro; IPR003502; Interleukin_1_prop.
Pfam; PF00340; IL1; 1.
Pfam; PF02394; IL1_propep; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO0264; INTERLEUKIN1.
SMART; SM00125; IL1; 1
PROSITE; PS00253; INTERLEUKIN_
STRAIN=2665 / ArCC 700392;

STRAIN=2695 / ArCC 700392;

STRAIN=2695 / ArCC 700392;

Tomb J.-F. White O. Kerlavage A.R., Clayton R.A., Sutton G.G.,

Pleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.

Relson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,

Relson K., Quackenbush J., Zhou L., Kirkness E.F., Glodek A.,

Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,

MCKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,

MCKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,

MCKENNEY R., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,

Cotton M.D., Weldman J.M., Fujli C., Bowman C., Watthey L., Wallin J.

Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Helicobacter pylori (Campylobacter Bacteria; Proteobacteria; epsilon s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101
                                                                                                                                                                                                                             The complete genome sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            titles requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EEIIMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER SECRETORY PROTEINS.
SIMILARITY: BELONGS TO THE IL-1 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EEVIMK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Macrophage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109
98
137
265 7
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137
30521
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66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 24; DB pred. No. 77; 2; Mismatches
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N-LINKED (GLCNAC. . .) (POUR N-LINKED (GLCNAC. . .) 
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subdivision;
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77;
                                                                                                                                                                                                                                    pathogen Helicobacter
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RESULT RE
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INPP_BOVIN
J. 2017
P21327;
Ol-MAY-1991 (Rel. 18, Created)
T Ol-MAY-1991 (Rel. 18, Last sequence update)
T 20-AUG-2001 (Rel. 40, Last anotation update)
T 20-AUG-2001 (Rel. 40, Last anotation update)
T NOSITOL POLYPHOSPHATE 1-PHOSPHATASE (EC 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 5
                                                                                                                                        BIOCHEMISTRY 33:13164-13171(1994).

1. CATALYTIC ACTIVITY: D-MYO-INOSITOL 1,4-BISPHOSPHATE + HD-MYO-INOSITOL 4-PHOSPHATE + ORTHOPHOSPHATE.

1. ENZYME REGULATION: INHIBITED BY LI(+).

1. PATHMAY: PHOSPHATIOYL INOSITOL SIGNALING PATHWAY.

1. SUBUNIT: MONOMER.

1. SUBUNIT: MONOMER.

1. AUTHOROUS: ACTS ON INOSITOL 1,4-BISPHOSPHATE AND INISCELLANEOUS: ACTS ON INOSITOL 3,6-BISPHOSPHATE).

1. ATRIPHOSPHATE (FORMING INOSITOL 3,6-BISPHOSPHATE).

1. SIMILARITY: BELONGS TO THE INOSITOL MONOPHOSPHATASE FAM.
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
MEDLINE-95034747; PubMed-7947723;
York J.D., Ponder J.W., Chen Z.W., Mathews F.S., Majerus P.W.;
"Crystal structure of inositol polyphosphate 1-phosphatase at 2.3-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDITIE-91086555; pubMed-2175905; York J.D., Majerus P.W.; York J.D., Majerus P.W.; "Isolation and heterologous expression of a cDNA encoding inositol polyphosphate I-phosphatase."; Proc. Natl. Acad. Sci. U.S.A. 87:9548-9552(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chorddta; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LT 12
BOVIN
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PROSITE; PS00787; CHORISMATE_SYNTHASE_1; 1.

PROSITE; PS00788; CHORISMATE_SYNTHASE_2; 1.

PROSITE; PS00788; CHORISMATE_SYNTHASE_3; 1.

PROSITE; PS00789; CHORISMATE_SYNTHASE_3; 1.

Lyase; Aromatic amino acid biosynthesis; Complete SEQUENCE 365 AA; 40100 MM; 98ABC708E1909561 CR
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les 5; Conserv
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EEIIVR 292
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Pred. No. 1.1e+02;
1; Mismatches 0;
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(EC 3.1.3.57) (IPPASE) (IPP).
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GDIB_MC
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Best Local
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PIR; A39254; A39254.
PDB; IINP; 26-JAN-95.
InterPro; IPR000760; Inositol_P.
Pfam; PF00459; Inositol_P; 1.
PRINTS; PR00378; INOSPHPHTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1996 (Rel. 34,
20-AUG-2001 (Rel. 40,
20-AUG-2001 (Rel. 40,
RAB GDP DISSOCIATION 1
GDI2 OR RABGDIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOUSE
GDIB_MOUSE
P50397;
                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-94217740; PubMed-7513052;
Shisheva A., Suedhof T.C., Czech M.P.;
Cloning, Characterization, and expression of a novel gDP
dissociation inhibitor isoform from skeletal muscle.";
Mol. Cell. Biol. 14:3459-3468(1994)
Mol. Cell. Biol. 14:3459-3468(1994)
Mol. Cell. Biol. 14:3459-3468(1994)
Mol. Cell. Biol. Regulation of Most Rab
PROTEINS. BY INHIBITING THE DISSOCIATION OF GDP FROM THEM, AND
SUBSEDUENT BINDING OF GTP TO THEM.

1- SUBCELJULAR LOCATION: CYTOPLASMIC AND MEMBRANE-ASSOCIATED.

1- TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED.
PRINTS; PRO0891; RABGDIREP
PRINTS; PR00892; RABGDI.
GTPase activation.
SEQUENCE 445 AA; 50512 N
                                                                                                                                                       HSSP; P21856; IGND
MGD; MGI:99845; Gdi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GDIZ or Namor (Mouse).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Eukaryota; Metharia; Rodentia;
                                                                        InterPro; IPR002005; Rab_GDI_REP.
'fam; PF00996; GDJ; 1.
'RINTS; PR00Re'
                                                                                                                                                                                                              EMBL; U07951; AAB16908.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-Skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hydrolase; Lithium; 3D-structure.
CONFLICT 84 84 L ->
SEQUENCE 400 AA; 43931 MW; CE
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90 EKIIMR
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40, Last sequence update)
40, Last annotation update)
10N INHIBITOR BETA (RAB GDI BETA) (GDI-2).
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Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; | Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -> F (IN REF. 1; AA SEQUENCE).
CF385265E4C674AA CRC64;
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/ Murinae; Mus
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50512 MW;

7FFD92EAE950EE49 CRC64;

RESULT

256 EETIMO 1 EEIIMR

6

Query Match Best Local S Matches

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fanning S., Leahy M., Sheehan D.;
"Nucleotide and deduced amino acid sequences of Rhizobium meliloti
102p34 lac2 gene: comparison with prokaryotic beta-galactosidases human beta-glucuronidase.";
Gene 141:91-96(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BGAL_RHIME STANDARD; PRT; 755 AA. 059750; 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation updat
ENV_HVIND STANDARD; PRT; 846 AA. P1879; O1-NOV-1990 (Rel. 16. Created) O1-NOV-1990 (Rel. 16. Last sequence update) 15-UL-1999 (Rel. 18. Last annotation update) ENVELOPE POLYPROTEIN GP160 PRECURSOR (CONTAINS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL, NON-REDUCIN
GALACTOSE RESIDUES IN BETA-D-GALACTOSIDES.
-1- SIMILARITY: BELONGS TO FAMILY 2 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94215895; PubMed=8163182; Fanning S., Leahy M., Sheehan D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L20757; AAA26296.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nterPro; IPR001649;
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Similarity 66.7%;
4; Conservative
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5; Conser
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PS00719; GLYCOSYL_HYDROL_F2_1;
PS00608; GLYCOSYL_HYDROL_F2_2;
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382 382 P.

463 463 N

755 AA; 84148 MW;
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Pred. No.
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NUCLEOPHILE (BY SIMILARITY).
, 09E339A92CC0D366 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spire B., Sire J., Zachar V., Rey F., Barre-Sinoussi F., Galibert F., Hampe A., Chermann J.C.;
"Nucleotide sequence of HIVI-NDK: a highly cytopathic strain of the human immunodeficiency virus.";
Gene B1:275-284(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000328; Env_GP41.
InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Polyprotei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M27323; AAA44873.1; -:
PIR; JQ0066; VCLJND.
HIV; M27323; ENV$NDK.
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NCBI_TaxID=11695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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AIDS, AND IS A HIGHLY CYTOPATHOGENIC STRAIN.
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                                                              Polyprotein; Glycoprotein; Transmembrane;
           85.7%;
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TRANSMEMBRANE GLYCOPROTEIN.
BY SIMILARITY.
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             ВВ
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NCBI\_TaxID=382;

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ENV\_HV1ND
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1 EEIIMR 6 |||:|: 551 EEIVMK 55

Hydrolase;
ACT\_SITE
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PROSITE;

Pfam;

PF00703;

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Post-processing: Minimum Match 0%
Maximum Match 100%
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Maximum DB
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1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
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11:135 Million cell updates/sec
 473505 seqs, 146272329 residues
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Gapop 10.0 , Gapext 0.5
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Q9PC67
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O70481 mus musculu
O27216 methanobact
Q55923 synechocyst
Q992y8 streptococc
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oppc67 xylella
oppf59 human
oppf59 human
oppgs21 human
oppgs21 human
oppgs45 human
oppd45 human
oppd469 human
oppe469 human
oppe465 human
oppe464 human
oppe464 human
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oppe466 human
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Q9E4D5	Q9E4E9	Q9E4F6	Q9E4H4	Q9E4H7	Q9E4G4	Q9E4C2	Q9E4D8	Q9E4G1	Q9E4C4	Q9E4D3	Q9E4D4	Q9E4D9	Q9E4E0	Q9E4E4	Q9E4E5	Q9E4E7	Q9E4E8	Q9E4H1	Q9E4H2	Q9E4H3	Q9E4G2	Q9E4G7	Q9E4G8	Q9E4C9	Q9E4G5
Q9e4d5 human immu	Q9e4e9 human immur	Q9e4f6 human immur	Q9e4h4 human immur	Q9e4h7 human immur	Q9e4g4 human immur	Q9e4c2 human immun	Q9e4d8 human immur	Q9e4gl human immur	human	Q9e4d3 human immur	Ξ.	human :	human			human	human	Q9e4hl human immur	Q9e4h2 human immur	Q9e4h3 human immur		Q9e4g7 human immur	Q9e4g8 human immu	Q9e4c9 human immur	Q9e4g5 human immur
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## ALIGNMENTS

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PRESULT 1

OPH970 PRELIMINARY; PRT; 401 AA.

C 99H970;

OT -MAR-2001 (TEMBLIFEL 16, Created)

DT 01-MAR-2001 (TEMBLIFEL 16, Last sequence update)

DE CDNA FL212968 FIS, CLONE NT2RP2005815.

OS Homo sapiens (Human).

ON NCBL_TAXLD-9600;

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MEDLINE-99037514; PubMed-9371463;

MEDLINE-99037514; PubMed-9371463;

Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., DuBois Smith D.R., Doucette-Stamm L.A., DeLoughery C., Gilbert K., Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safter H., Patwell D., Prabhakar S., John A., Bush D., Safter H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pletrovski S., Church G.M., McDougall S., Shimer G., Goyal A., Pletrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.;

"Complete genome sequence of Methanobacterium thermoautotrophicum deltah: functional analysis and comparative genomics.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kwon Y.T.,
Sangan P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00396; ZnF_UBR1; 1.
PROSITE; PS00732; RIBOSOMAL_S16;
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Kwon Y.T., Reiss Y., Fri
Sangan P., Copeland N.G.
Submitted (APR-1998) to
                                                                                                                                                               Archaea; Euryarchaeota;
Methanothermobacter.
                                                                                                                                                                                                              CONSERVED
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Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
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Mammalia; Eutheria;
                                                                                                                              EQUENCE FROM N.A.
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IPR003126; ZnF_UBR1.
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N.G., Jenkins N.A., V
genes encoding the
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HYPOTHETICAL 28.8 KDA PROTEIN.
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Hosouchi
Streptococcus pyogenes.
Bacteria; Firmicutes; Bacillus/Clostridium
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EMBL: D64005; BAA106861; ---
EMBL: D64005; BAA106861; ---
SEQUENCE 263 AA; 28752 MW; 2FDE130FA3820763
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Tabata
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MEDLINE-96127529; pubmed-8590279;

Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T.,

Sugiura M., Tabata S.;

Sugiura M., Tabata S.;

Sequence analysis of the genome of the unicellular

Synechocystis sp. strain PCC6803. I. Sequence featur

region from map positions 64% to 92% of the genome.*

DNA Res. 2:153-166(1995).
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EMBL; AE000884; AAB85637.1; -.
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SEQUENCE 157 AA; 17145 MW; 7EA
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   group; Streptococcaceae;
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RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa N.C.R., Costa N.C., El Dorry H.,
RA Facincani A.P., Ferreira A.J.S., Ferretra V.C.A., Ferro J.A.,
RA Facincani A.P., Ferreira A.J.S., Ferretra V.C.A., Ferro J.A.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Kitajima J.P.,
RA Kiteger J.E., Kuranae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Kiteger J.E., Kuranae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Marques M.Y., Martins E.M.F., Matsukuma A.Y.,
RA Marques M.Y., Martins E.A.L., Martins E.M.F., Mathado J.A.,
RA Mandado M.A., Madeira A.M.B.N., Madeira H.M.F., Matsukuma A.Y.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Matis A.J., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Silva A.C.R., de Silva R.R., Santelli R.V., Sawasaki H.E.,
RA de Rosa V.E. J.T., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA de Silva A.C.R., de Silva R.M., Jasiba S.M., Tsuhako M.H.,
RA de Silva A.C.R., de Silva R.M., Jasiba S.M., Tsuhako M.H.,
RA da Silva A.C.R., de Silva R.M., Jasiba S.M., Tsuhako M.H.,
RA da Silva A.C.R., de Silva R.M., Verjovski Almeida S.M., Tsuhako M.H.,
RA de Rosa V.E. J.Silva R.A., Verjovski Almeida S.M., Tsuhako M.H.,
RA Mathada H., Van Sluys M.A., Verjovski Almeida S.M., Tsuhako M.H.,
RA Mathada H., Van Sluys M.A., Verjovski Almeida S.M., Tsuhako M.H.,
RA Mathada H., Van Sha Sha Sha Sha 
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Ferretti J.J., McShan W.M., Ajdic D.J., Savic G., Lyon K.,
Ferretti J.J., McShan W.M., Ajdic D.J., Savic G., Lyon K.,
Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J.,
Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
"Complete genome sequence of an M. Strain of Streptococcus pyogenes.";
Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
EMBL; AE006546; AAK33910.1;
EMBL; AE006546; AAK3910.1;
BYDOTHETICAL PROFERI, Complete Proteome.

Hypothetical profesi; Complete Proteome.
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01-OCT-2000 (TEMBLIE1. 15, Last sequence update)
01-UN-2001 (TEMBLIE1. 17, Last annotation update)
ANTHRANILATE SYNTHASE COMPONENT I.
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NCBI_TaxID-1314;
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Submitted (SEP-2000) to the EMBL/Geniembi; AF309426; AAG49507.1;
NON_TER 1 1
NON_TER 71 71 71
SEQUENCE 71 AA; 7927 MW; 3DDBA8E1
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099F59;
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01-JUN-2001
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PRINTS; PR00095; ANTSNTHASEI.
ProDom; PD000779; Chorismate_bind;
Complete proteome.
SEQUENCE 498 AA; 56109 MW; 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O73207 PRELIMINARY; PRT; 81 AA.
073207;
01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ENVELOPE GLYCOPROTEIN (FRAGMENT).
                                                                           Roques P.;
Submittled (MAY-1998) to the
EMBL; AJ006737; CAA07211.1;
InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
                                                                                                                                                                                                                                                                                                                                                       Human immunodeficiency virus type 1. Viruses; Retroid viruses; Retroviridae; NCBI_TaxID-11676;
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-SAMPLE CAMOO1B;
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Viruses; Retroid viruses; Retroviridae;
NCBI_TaxID=11676;
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1.1e+02;
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GLYCOPROTEIN :
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  "Highly variable sequences at env V3 region of among Thai carriers during 1955 to 1997."; Submitted (AUG-1999) to the EMBL/GenBank/DDBJ dEMBL; AB031954; BAA83904.1; ... InterPro; IPR000777; GP120. Pfam: PF00516; GP120: 1.
                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-97RVT592;
STRAIN-11 W., Ayuthaya P.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Highly variable sequences at env V3 region of HIV-1 distributing among Thai carriers during 1995 to 1997."; Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AB031918; BAA83868.1; InterPro; IPR000777; GP120. Pfam: PP00516; GP120: 1.
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Viruses; Retroid viruses; Retroviridae; Lentivirus
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STRAIN-95TNIH322;
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5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99 AA;
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) (TrEMBLrel. 13, 1
L (TrEMBLrel. 17, 1
LN 120 (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
N 120 (FRAGMENT).
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                                                                                                                                                                                 Duangchanda
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 25; DB Pred. No. 1.5e 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8C1275D499E96982 CRC64;
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1.5e+02;
hes 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 12;
1.2e+02;
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                                                                                                                                                                                 Mukai
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                                                                                                                                       HIV-1
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                                                                                                                                                                                 Kurata
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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Best Local S
Matches 5
                           SEQUENCE FROM N.A.

STRAIN-SUBTYPE E;

STAIN-SUBTYPE E;

Sato H., Shino T., Kodaka N., Taniguchi K., Tomita Y.,

Miyakuri T., Takebe Y.;

"Evolution and biological characterization of human important the strain of the sequences following howering to the strain of the sequences following howerical virus transmission in a single family.";

Vertical virus transmission in a single family.";

J. Virol. 0:0-0(1998).

R EMBL; ABOUL4805; BAA74625.1;

R InterPro; IPR000777; GP120.

R Pfam; PF00516; GP120; 1.
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Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                   O9YN32 PRELIMINARY;

O9YN32;

01-MAY-1999 (TrEMBLrel. 10, C

01-MAY-1999 (TrEMBLrel. 10, L

01-JUN-2001 (TrEMBLrel. 17, L

ENVELOPE GLYCOPROTEIN GP120 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN PATIENT 8;
Leroux C.;
Leroux C.;
"HIV-1 shedding.";
submitted (APR 2000) to the EMBL/GenBank/DDBJ
EMBL; AF256462; ARG16123.1;
InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
NON_TER
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Q9E4C3;
Q1-MAR-2001 (TrEMBLrel. 16, Created)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Q1-JUN-2001 (TREMBLREL. 17).
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SEQUENCE
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NON_TER
SEQUENCE
Envelope protein.
                                                                                                                                                                                                                                                                                                            Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae;
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
NCII_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EEIIMR 6
||||:|
2 EEIILR 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          102 AA;
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10795 MW;
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Last sequence upo
Last annotation of 
(FRAGMENT)
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1; Mismatches
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Pred. No. 1.6e
1; Mismatches
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1.6e+02;
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1.5e+02;
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(on update)
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                                                                                                                                                                                                                            Kato K.,
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Best Local S
Matches 5
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Best Local Similarity 83.
Matches 5; Conservative
Query Match
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leroux C.;
"HIV-1 shedding.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ EMBL; AF256426; AAG16087.1; -.
Interpro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID-11676;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ENVELOPE GLYCOPROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9E4F8
                                                                                                                                              "HIV-1 shedding.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF256427; AAG16088.1; -.
InterPro; IPR000777; GF120.
Pfam; PF00516; GP120; 1.
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-PATIENT 8;
                                                                                                                                                                                                                                                                                                                                                                                                         luman immunodeficiency virus type 1.
/iruses; Retroid viruses; Retroviridae;
(CBI_TaxID=11676;
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||||:|
14 EEIILR 19
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11-MAR-2001 (TrEMBLrel. 16, Last sequence update)
11-UN-2001 (TrEMBLREL. 17, Last annotation update)
NVELOPE GLYCOPROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9E4F8;
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5; Conservative
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107 AA;
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                                                                                      107 AA;
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12305
                                                                                         12032 MW;
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      89.38;
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Pred. No. 1.7e+02;
1; Mismatches 0;
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      Score
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                                                                                            2E274D8528E39E9E CRC64;
      25;
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      DB 12;
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Query Match
Best Local Similarity
Watches 5; Conserve
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Q9E4F5;
Q1-MAR-2001 (TrEMBLrel. 16, Created)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ENVELOPE GLYCOPROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leroux C.;
"HIV-1 shedding.";
"HIV-1 shedding.";
"Leroux G.;
"HIV-1 shedding.";
"Holding.";
"Holding."
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCDI_TaxID=11676;
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STRAIN-PATIENT 8;
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2 EEIILR 7
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1; Mismatches
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Pred. No. 1.7e+02;
1; Mismatches 0
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